



MAJORITY ATGXXGGCGATGCTTCCCTCTTTGAGCCCAAAGCCGGGTCTCTCTGGTGACGGGCACACCTGGCCT

DNAPTAQ ...AG..G.....G..... 70
DNAPTFLC.G..... 67
DNAPTTH ...GA.....A..... 70

MAJORITY ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCACCGGGGGAACCGGTGCAGGGGTCTACGGCTT

DNAPTAQCA.....G.G..... 140
DNAPTFLT.....C.....C.T..... 137
DNAPTTHG..... 140

MAJORITY CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGGACXXGCCGGTGXTCGTGGTCTTTGACGCCAAG

DNAPTAQC.....A..... 207
DNAPTFLA.....GT..T..... 204
DNAPTTHT..AA..C..CT..... 280

MAJORITY GCCCCTCCTTCCGCCACGAGGCCTACGAGGCCTACAAGGGGGCCGGGCCCCACCCCGGAGGACTTTC

DNAPTAQG..GG.....G..... 277
DNAPTFL 274
DNAPTTHGA.....G.....C..... 280

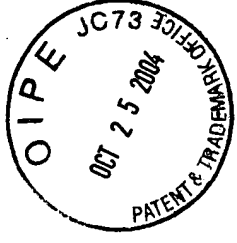
MAJORITY CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGACCTCCTGGGGCTTGCGCGCCTCGAGGTCCCCGGCTA

DNAPTAQA.....G.....G..... 347
DNAPTFLG.....T.....A.C.....T..G..G.....T..... 344
DNAPTTH 350

FIG. 1A

MAJORITY	CGAGCGGACGACGT	XCTGGCCACCCTGGCC	AAGAAGGCGGAAAGGAGGGGTACGAGGTGCGGCATCCTC	
DNAPTAQC.....G.....C.....C.....	417
DNAPTFL	T.....G.....CG.....	414
DNAPTTHT.....C.....	420
MAJORITY	ACGCGCGACCGACCTCT	ACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA		
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G..G.....A.....T.....	484
DNAPTTH	A..G.C.....G.....CC.....	490
MAJORITY	TCACCCCGCGGTGGCTTT	GGGAGAAGTACGGCCTGAGGCCGCGAGCAGTGGGTGGACTACCGGGCCCTGGC		
DNAPTAQC.....	A.....C..C.....	557
DNAPTFLAC.....C.C.....	554
DNAPTTHA.....C.....T..C.....	560
MAJORITY	GGGGGACCCCTCCGACAACCT	CCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCCGGAGCTCCTCXAG		
DNAPTAQ	C.....GAG.....	T.....G..GAG.....	627
DNAPTFLG..T..A.....G.....A..G.....	624
DNAPTTHTC.....	630
MAJORITY	GAGTGGGGAGCCTGGAAACCT	CCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCCGGGAGAAGA		
DNAPTAQGC.....C.....A.....	694
DNAPTFL	T..C..C.....A.....T.....	691
DNAPTTHA.....	A..AAA..G.....	700

FIG. 1B



MAJORITY TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCCAGGTGGCACCACCGACCTGCCCCCTGGA

DNAPTAQC..T...A.....C..GG..A..... 764
DNAPTFLGGG.....G.C...GCC..T...C..A...T...A...T..... 761
DNAPTTHA.....C.....A.....C.G.....T.....C.....C..... 770

MAJORITY GGTGGACTTCGCCAAGXGGCGGGAGGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT

DNAPTAQAA.....AA.....A.....A.....T.....T.....T..... 834
DNAPTFLGG.G.C.C.C.CACA...A...T.....T...GC...T...T...C..T..... 831
DNAPTTHC.....C..G.....C.....C.....C.....C.....C..... 840

MAJORITY GGCAGCCTCCTCCACGAGTTCGGCCTCCTGGAGGGGCCCCAAGGCCCTGGAGGAGGCCCTGGCCCCCGC

DNAPTAQT.....AA.....T.....AA..... 904
DNAPTFLA.....G.....G.....G.....GCA.....T..... 901
DNAPTTHC.....C.....C.....GCC..... 910

MAJORITY CGGAAGGGCCCTTCGTGGGCTTTGTCCCTTTCCCGCCCCGAGCCCATGTGGGCCGAGCTTCTGGCCCTGGC

DNAPTAQG.....AAG.....T..... 974
DNAPTFLT..TT.....TC.T.....T.....G..... 971
DNAPTTHC.....C.....C.....AAA..... 980

MAJORITY CGCCGCCAGGGGCGGGTCCACCGGGCACCAACCCCTTTAXGGGCCCTXAGGGACCTXAAGGAGGTG

DNAPTAQG.....C..C..G..T.A..AA.C..C.....G.....C. 1044
DNAPTFL T.GG..GT.....G..CC...T.....A.....C.....G.....T.....G..... 1041
DNAPTTHTG.....C.....G.....G.....G..A.A.....C.....C 1050

FIG. 1C

MAJORITY CGGGGXCTCCTCGCCAAGGACCTGGCCGTTTGGCCCTGAGGGAGGCGCTXGACCTCXTGCCCGGGGACG

 DNAPTAQG..T.....A.....AG.....C.....T.G.....CC.....C..... 1114
 DNAPTFLAA.....G.....G.....C.....G.....T.C..A.A..... 1111
 DNAPTTHC.....C.....C.....TC.....G..A.....G..... 1120

 MAJORITY ACCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACACCCCGAGGGGTGGCCCGGCTACGG

 DNAPTAQT.....T.....T.....T.....T.....T..... 1184
 DNAPTFLG.....T.....T.....T.....T.....T..... 1181
 DNAPTTHG.....G.....G.....G.....G.....G..... 1190

 MAJORITY GGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG

 DNAPTAQ C.....G.....G.....GC...T.....GCC.....GTG..G. 1254
 DNAPTFLT.....A.....GG.....C.C.....A..C...AA... 1260
 DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

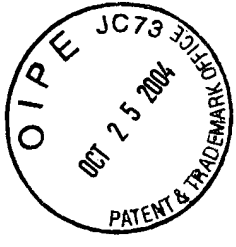
 MAJORITY CGCCTTGAGGGGAGGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCCCTTCCCGGGTCCIGG

 DNAPTAQ A.G.....G.....G.....G.....G.....GCT..... 1324
 DNAPTFLA...A..A.C.C.G.....G.....G.....GT... 1321
 DNAPTTHC.....A.....C.....C.....A.....C..... 1330

 MAJORITY CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

 DNAPTAQG..C.....G..C.....T...AG....T.G.....C... 1394
 DNAPTFLGG.....C.....C.....C.....C.....A..C 1391
 DNAPTTHC.....A.....A.....T.....T.....C.T..... 1400

FIG. 1D



MAJORITY GGAGATCCGGCCCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC

DNAPTAQGC.....CC..... 1464
DNAPTFLG.G....AG..G..... 1461
DNAPTTHT.....G..... 1470

MAJORITY CAGCTGGAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC

DNAPTAQC.....A.....C..... 1534
DNAPTFLGC.....G..C..G..T.....G..G..A. 1531
DNAPTTHTA.....T.G..G.....C.A.....A..... 1540

MAJORITY GCTCCACGAGCGCCGTGCTGGAGGCCCTXCGXGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQC.....C..... 1604
DNAPTFLT.....G..A.....CCGC..... 1601
DNAPTTHG.....A..G.....C...C. 1610

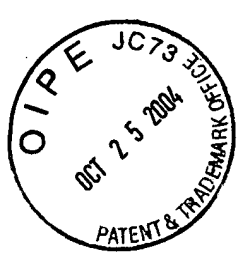
MAJORITY CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCXGXCTCGTCCACCCAGGACGGGC

DNAPTAQG....G.....T....G.A...A..... 1674
DNAPTFLA.....C.C...G.....A...C... 1671
DNAPTTHG.G.....AAG.....G..... 1680

MAJORITY CGCCTCCACACCCGCTTCAACCAGACGGCCACGGGCAGGGCTTAGTAGCTCCGACCCCAACCTGC

DNAPTAQA.....T.....C. 1744
DNAPTFLG.....C.....TCC..... 1741
DNAPTTHG.....G..... 1750

FIG. 1E



MAJORITY AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCGGCCCTTCGTGGCCGAGGAGGGXGTGGGT

DNAPTAQG..T..G.....A.C.....G...C. 1814
DNAPTFLG.....C.C.....A.....C.....C..... 1811
DNAPTTHCT.....C.....T.....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTGGCCACCTCTCCGGGACGAGAACCTG

DNAPTAQ A.....A.....A...G.....C.....C..... 1884
DNAPTFL .C.....T.T.....C.....T.....A..... 1881
DNAPTTHC.....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGAGGGACATCCACACCCAGACCCGCGCTGGATGTTCCGGCTCCCCCGG

DNAPTAQC.....C.....GG.....G... 1954
DNAPTFLT.....A.....TT...C. 1951
DNAPTTH ...A.....A.....A..... 1960

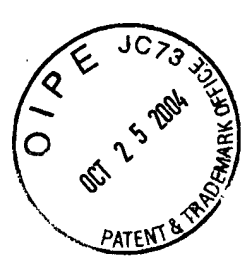
MAJORITY AGGCCGTGGACCCCTGATGCGCCGGCGGCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCCGC

DNAPTAQA.....T.....G... 2024
DNAPTFL .A.GG..A....T.....G.....G..... 2021
DNAPTTHGG.G.....C..... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCATCCCCCTACGAGGAGGCGGTGGCCTTCATTGAGCGCTACTTCCAG

DNAPTAQA.....T.....CCA.....T... 2094
DNAPTFLGG.....T.....T.....A..... 2091
DNAPTTH ...TA.G.....T.....A..... 2100

FIG. 1F



MAJORITY AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAAGACCCTGGAGGAGGGCAGGAGCGGGGTACGTGGGAGA

DNAPTAQ 2164
DNAPTFLA.....GG.....C.....C.CC.....T..... 2161
DNAPTTHA.....A.....G.....A.....C.....A..... 2170

MAJORITY CCCTCTTCGGCCGCGCGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAAGAGCGTGC GGGAGCGGCGGGA

DNAPTAQC.....A.....AG.G.....C..... 2234
DNAPTFLT.....C..... 2231
DNAPTTHAA.AA.....CA.....C..... 2240

MAJORITY GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCGACCTCATGAAGCTGGCCATGGTGAAGCTC

DNAPTAQT..... 2304
DNAPTFLG.....CG...T 2301
DNAPTTHC..... 2310

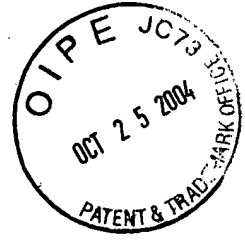
MAJORITY TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCTCTXCAGGTCCACGACGAGCTGGTCTCGAGGCC

DNAPTAQA...GG.....T..... 2374
DNAPTFLT...C.....G.....TT.G.....G..... 2371
DNAPTTHC..C.G...G.....C.C.....C.....CC...G..... 2380

MAJORITY CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAAGGAGGTGTCATGGAGGGGGTCTATCCCTGGCCGT

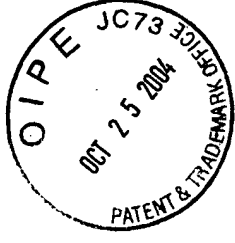
DNAPTAQA.....A.....CC.....CGGC.....G..... 2444
DNAPTFLG..C.....AG...A.....GG.....CAG... 2441
DNAPTTHC...C.....C...A.....G.....C.....AA..C.....C..... 2450

FIG. 1G



MAJORITY	GGCCCTGGAGGTGGAGGTGGGGGAGGAGTGGCTCTCCGCCAAGGAGTAG	
DNAPTAQA.....GA	2499
DNAPTFLCC.....	2496
DNAPTTHT.....GT...	2505

FIG. 1H



MAJORITY MXAMPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLLKALKEDG·DAVXVVFDAK

TAQ PRO .RG.....H.....I..... 69
TFL PROV.V..... 68
TTH PRO .E.....YK..F..... 70

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL

TAQ PROGG.....A.....S..... 139
TFL PROV.....F.....R..... 138
TTH PROFT..... 140

MAJORITY TADRDLYQLLSDRIAHLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSPDNLPGVKGIGEKTAAXLLX

TAQ PROK.....H.....D.A.....T.E.....R...E 209
TFL PROE..I.....Y.....A.....I.....QR..IR 208
TTH PROV..V.....H...E.....F..V.....L...K 210

MAJORITY EWGSLLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF

TAQ PROA.....L...AI...L...D..K..WD.AK.....K.....R..... 278
TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL..... 277
TTH PROENV...K..L...R..LE..R.....L.QG..... 280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAELLALAAARXGRVHRAXDPLXGLRDLKEV

TAQ PROS.....K.....D.....PE.YKA.....A 348
TFL PROG..A.....L..SF.....G.WE..L...Q...R.....G. 347
TTH PROA.AP.....K.....C.D.....A...A..K..... 350

FIG. 2A

MAJORITY RGLLAKDLAVLALREGDLXPDDPMLLAYLLDPSNTTPEGVARRYGGENTEDAGERALLSERLFXNLXX

TAQ PROS.....G.P.....E.....A.....A.....WG 418
TFL PRO ..I.....F.E.....A.....QT.KE 417
TTH PROS.....V.....AH.....HR..LK 420

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRDLVAYLQALSLEVAEEIRLEEEVFRLAGHPFNLNSRD

TAQ PROR...R...A.....R.....A.....A..... 488
TFL PRO ..K.....E.....R.....EA.V.Q..... 487
TTH PROK.....H.....L..... 490

MAJORITY QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILQYRELTKLKNITYIDPLPXLVHPRTG

TAQ PROR...L...Q.....H.....V.....S..... 558
TFL PRODR.....A...K... 557
TTH PROR...L...Q.....H.....V.....S..... 560

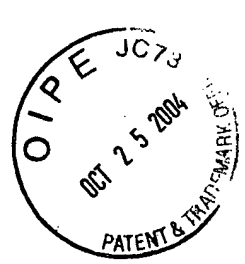
MAJORITY RLHTRFNQTATGRLSSSDPNLQNIPVRTPLGQIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

TAQ PROI.....L..... 628
TFL PROV.V..... 627
TTH PROA.A..... 630

MAJORITY IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVL YGMSAHLRSQELAIPEEAVAFIERYFQ

TAQ PROE.....R.....Q..... 698
TFL PROS.G.....G..S..... 697
TTH PROK.....V..... 700

FIG. 2B



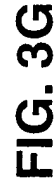
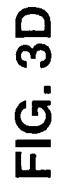
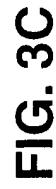
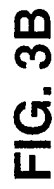
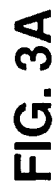
MAJORITY SFPKVRWIEKTL E E G R R R G Y V E T L F G R R R Y V P D L N A R V K S V R E A A E R M A F N M P V Q G T A A D L M K L A M V K L

TAQ PROE..... 768
TFL PROG.....R. 767
TTH PROK..... 770

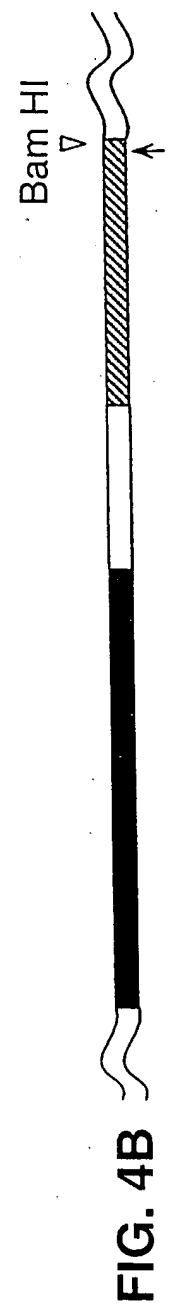
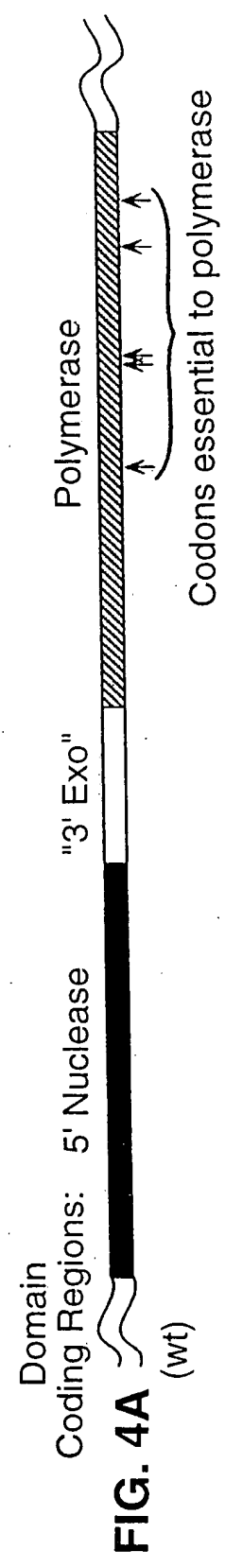
MAJORITY FPRLXEMGARM L L Q V H D E L V L E A P K X R A E X V A A L A K E V M E G V Y P L A V P L E V E V G X G E D W L S A K E X

TAQ PROE.....A..R.....I..... 833
TFL PROQ..L.....D...R.....W..Q.....L..... 831
TTH PROR.....L.....Q A...E.....A..K A.....M.....G 835

FIG. 2C



Genes for Wild-Type and Pol(-)DNAPTfl



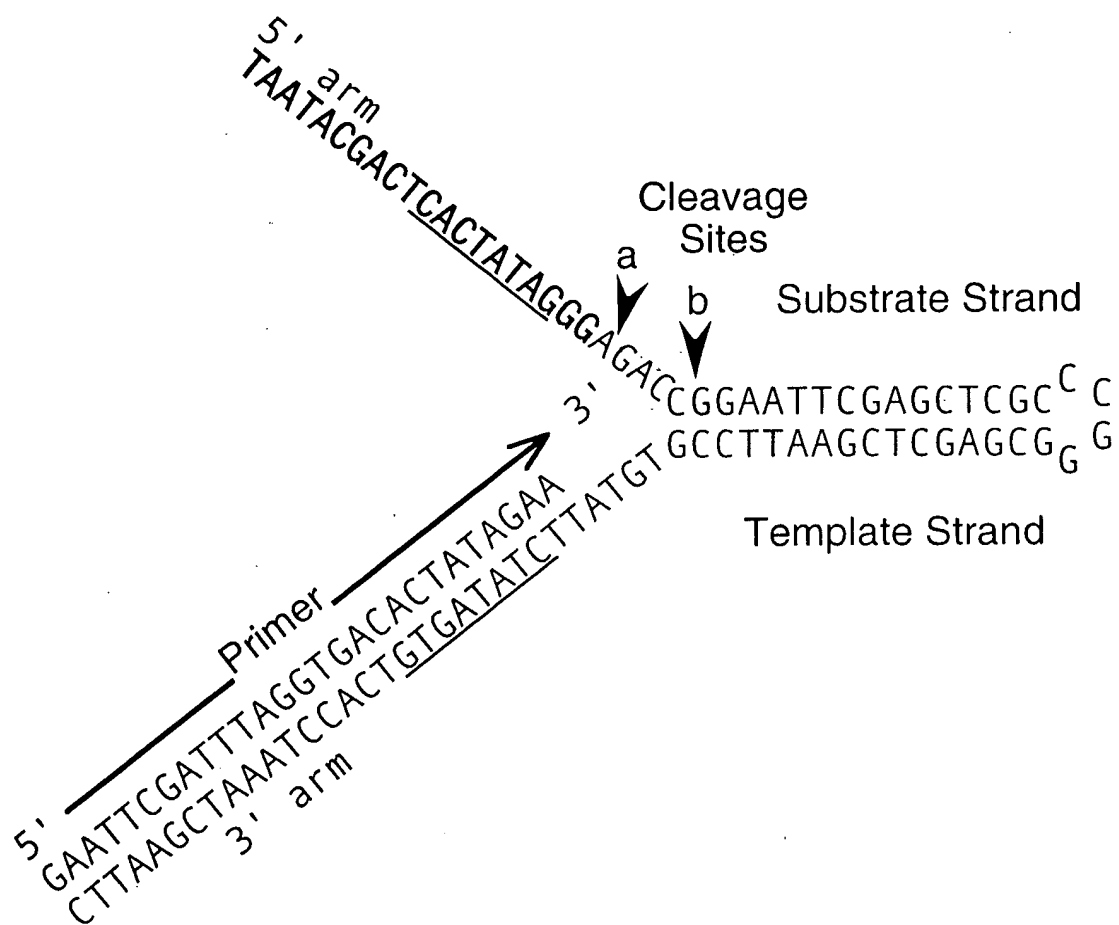
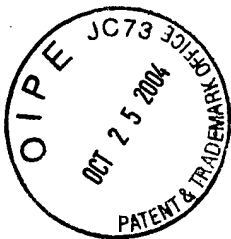


FIG. 5

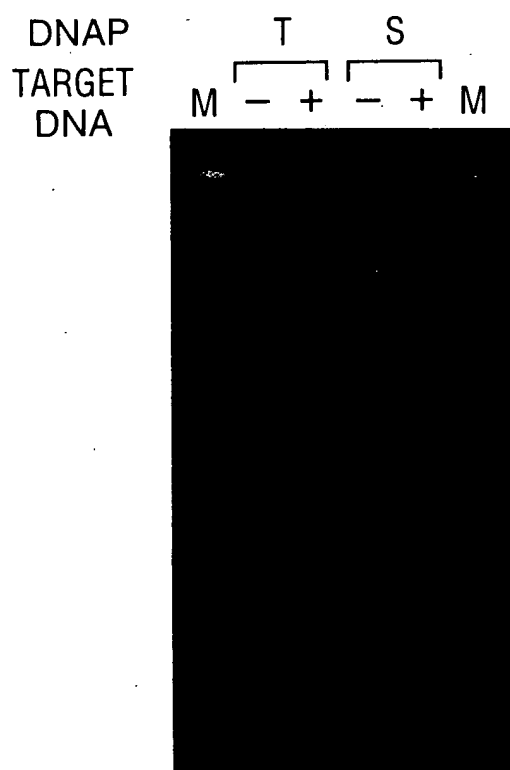
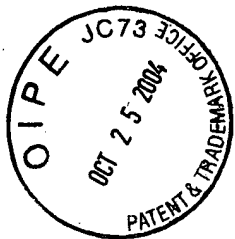


FIG. 6

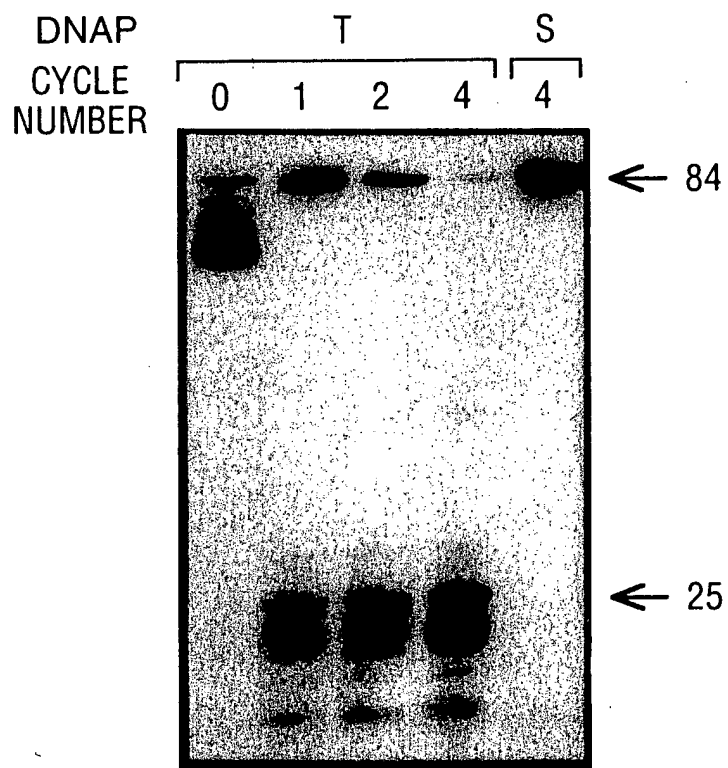
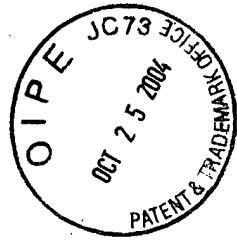


FIG. 7

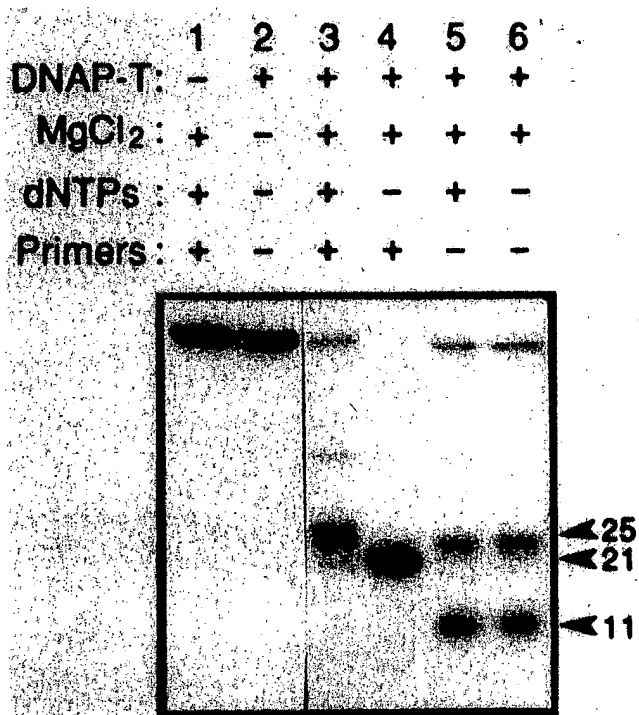


FIG. 8A

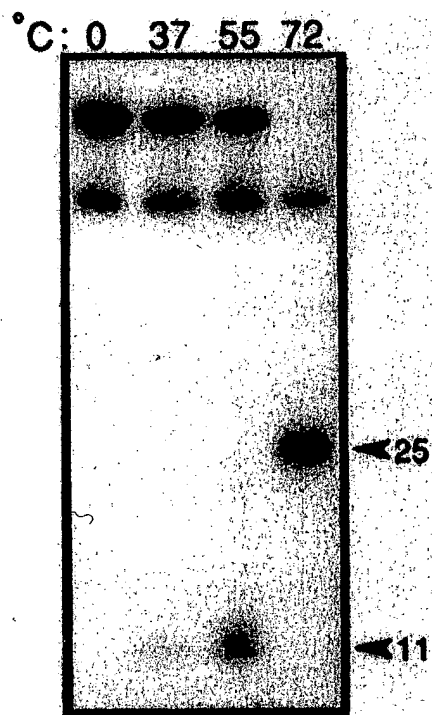


FIG. 8B

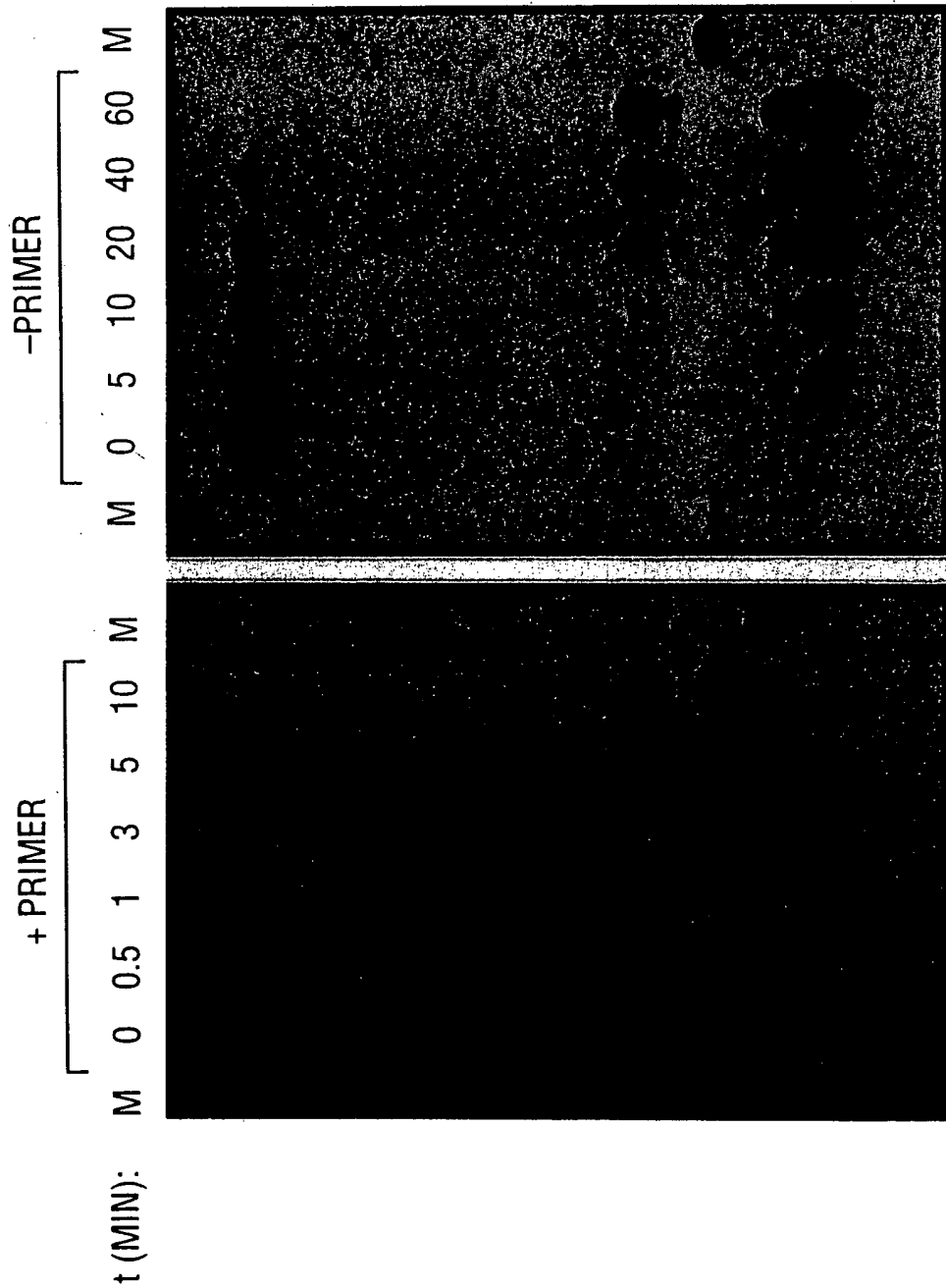


FIG. 9A

FIG. 9B

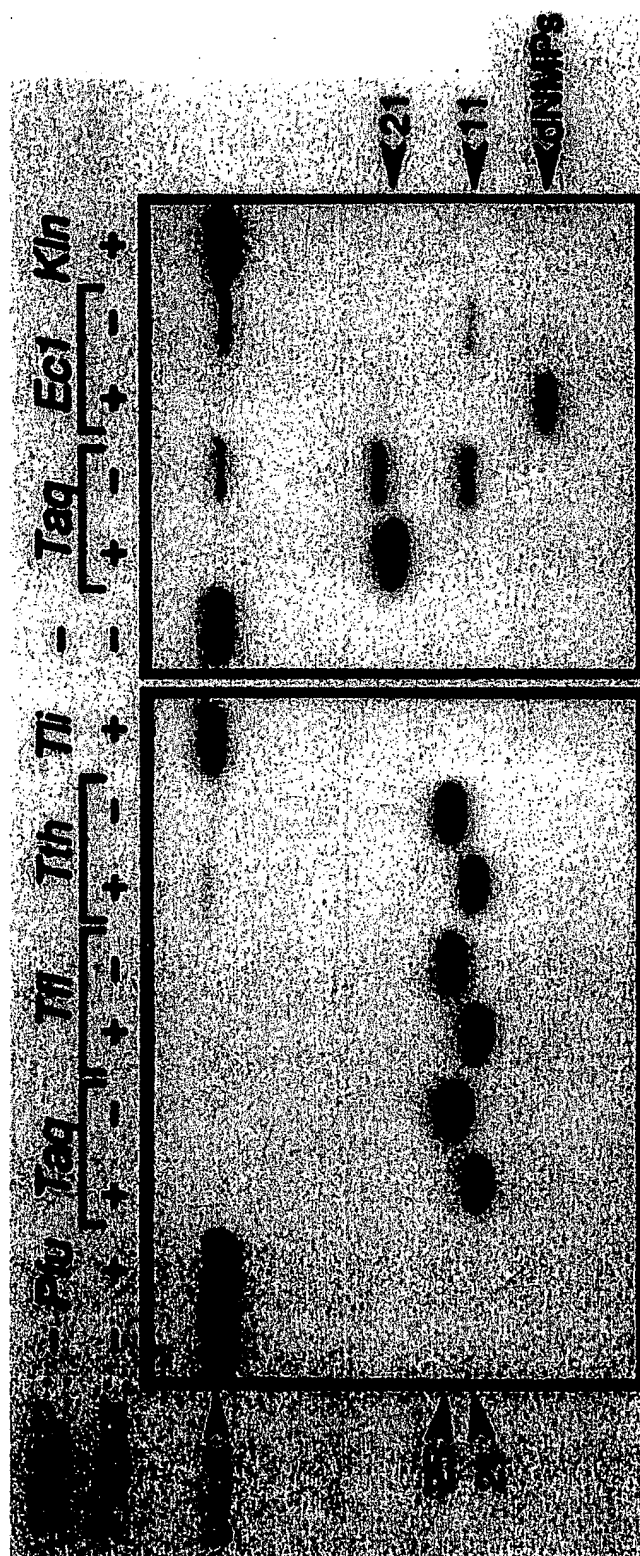


FIG. 10B

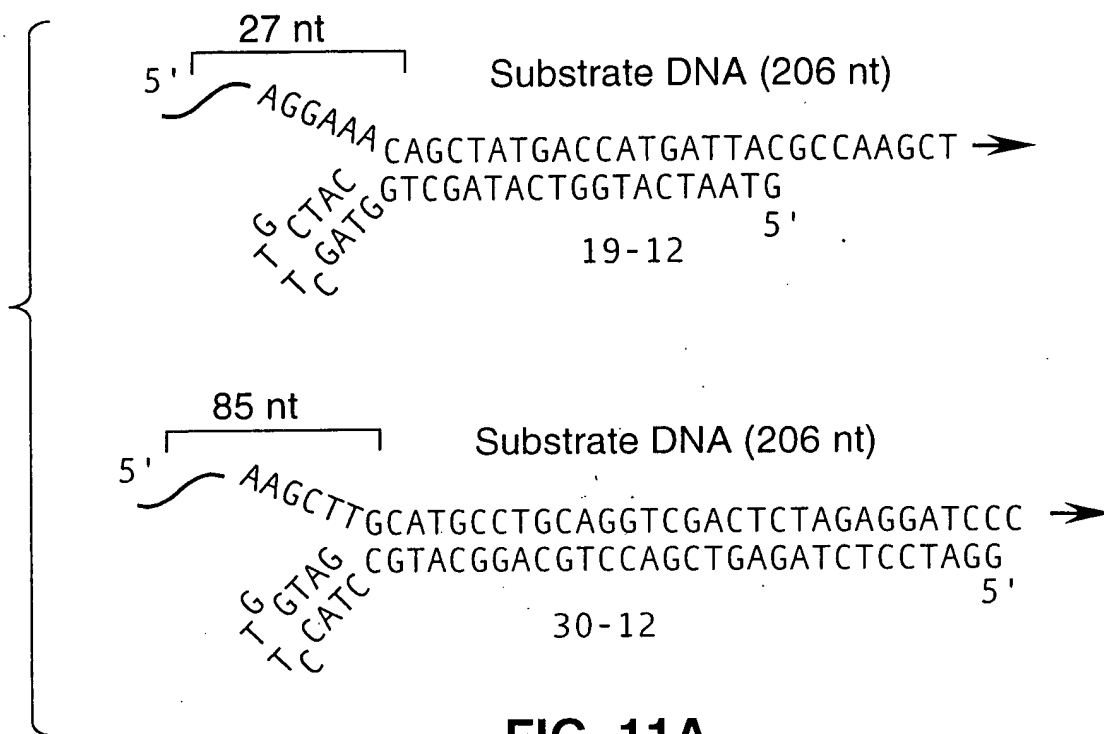
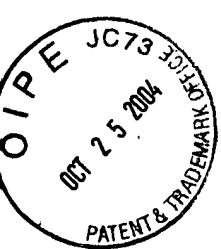


FIG. 11A

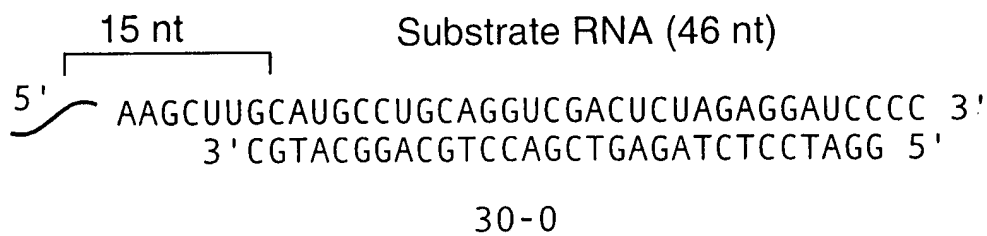


FIG. 12A

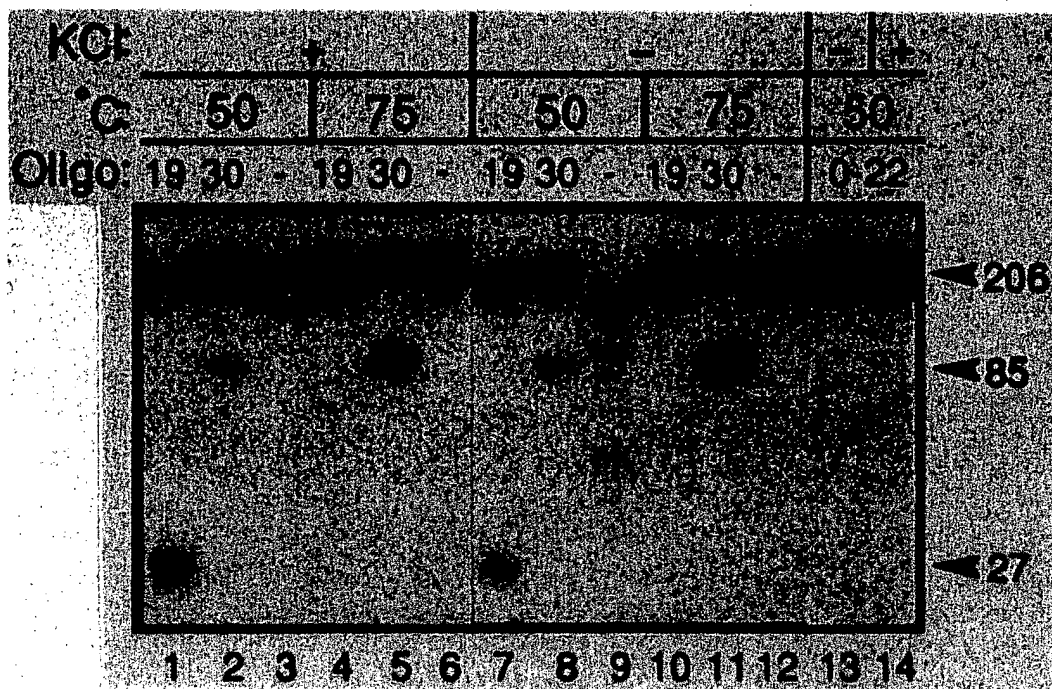


FIG. 11B

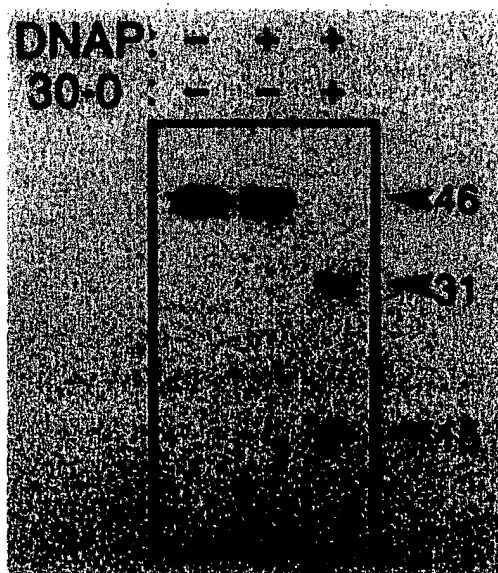
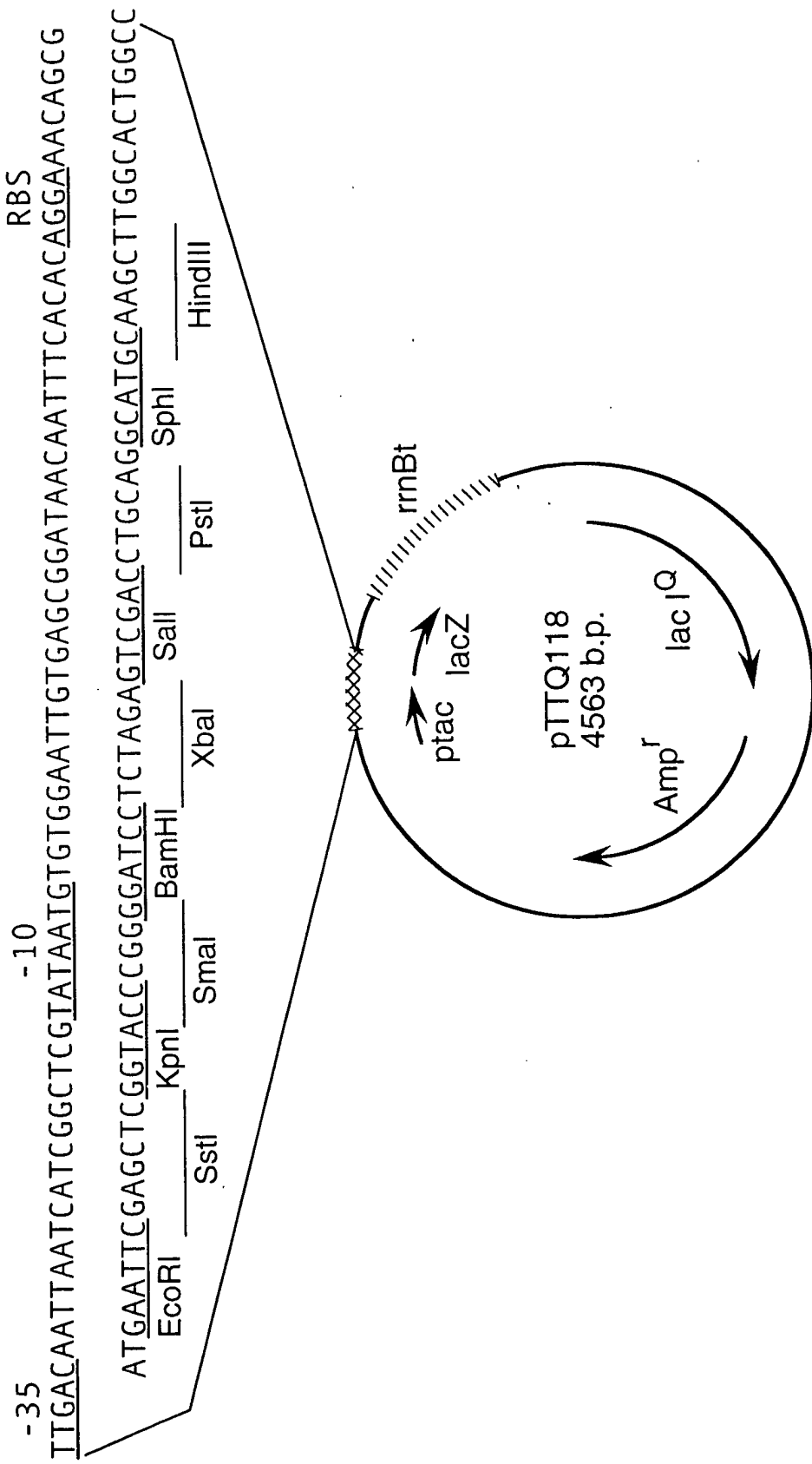
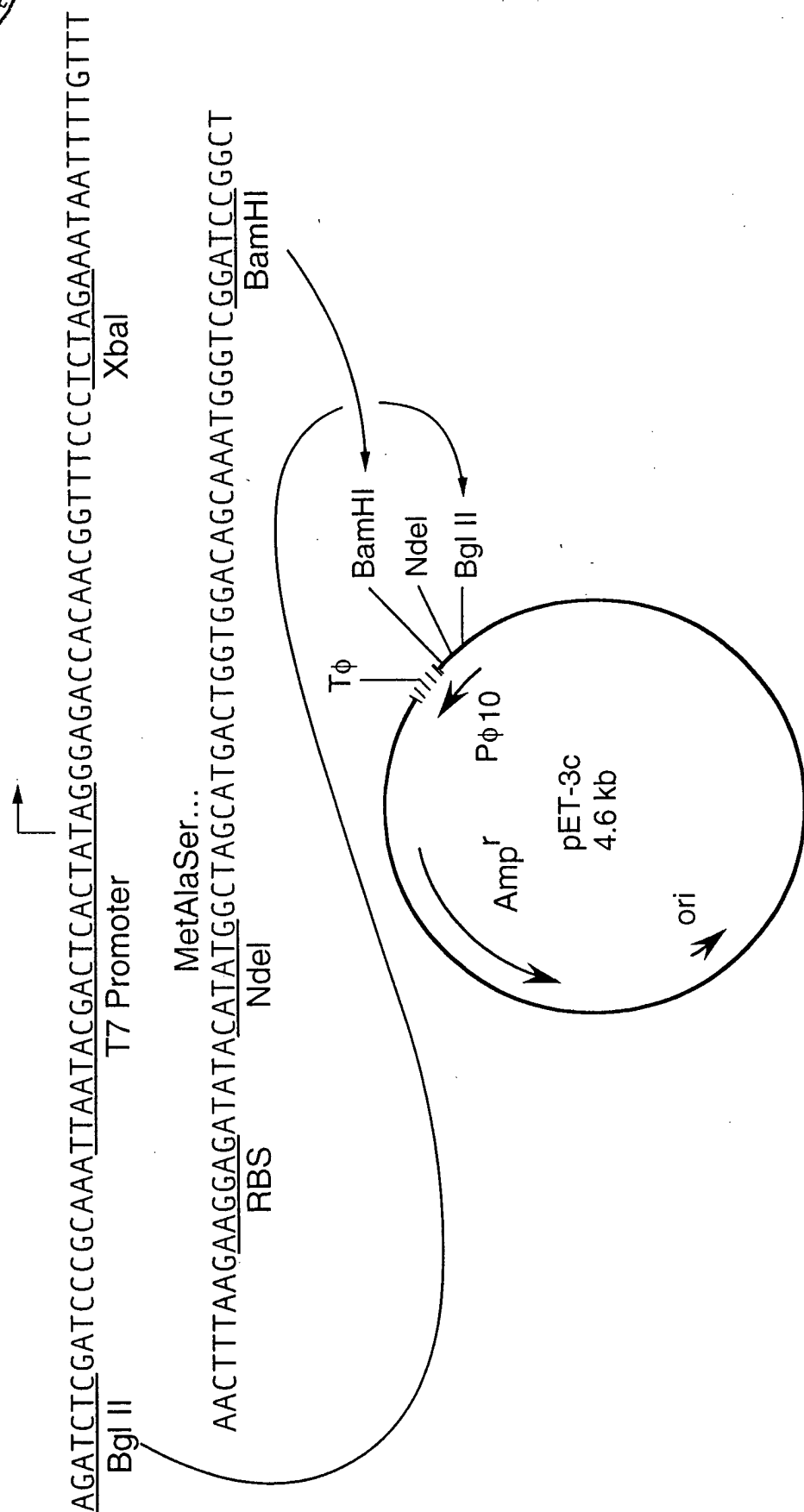


FIG. 12B



RBS: Ribosome binding site
 ptac: Synthetic tac promoter
 lac I^Q: Lac repressor gene
 lacZ: Beta-galactosidase alpha fragment
 rrnBt: E. coli rrnB transcription terminator

FIG. 13



P_{φ10} : Bacteriophage T7 φ10 promoter RBS: Ribosome binding site
 T_φ: T7 φ Terminator

FIG. 14

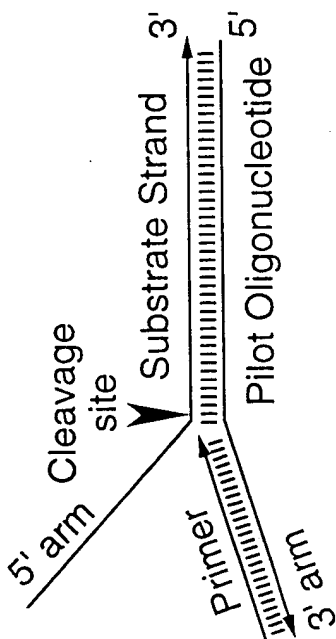


FIG. 15B

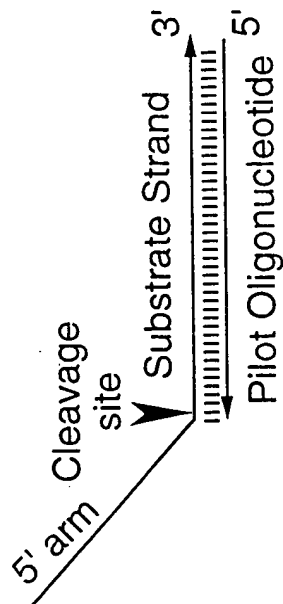


FIG. 15D

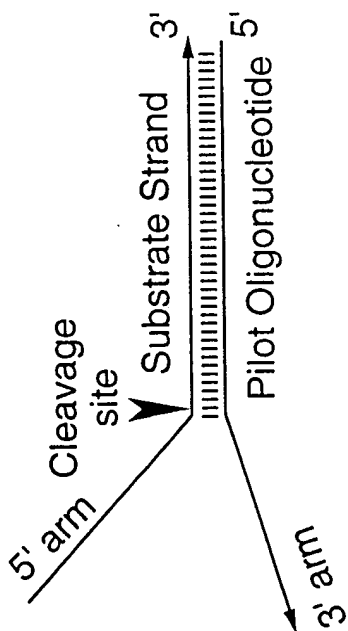


FIG. 15A



FIG. 15C

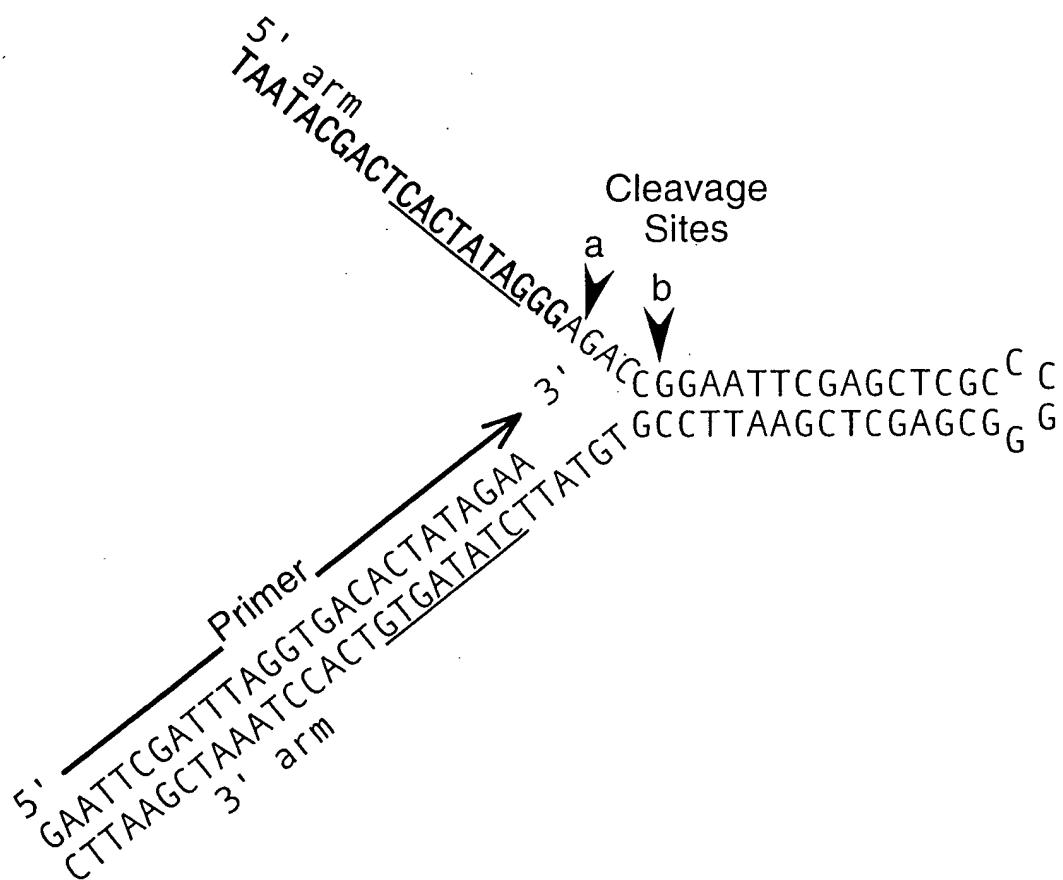
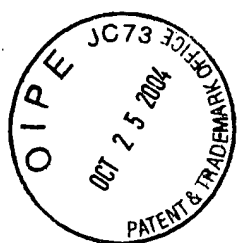


FIG. 15E

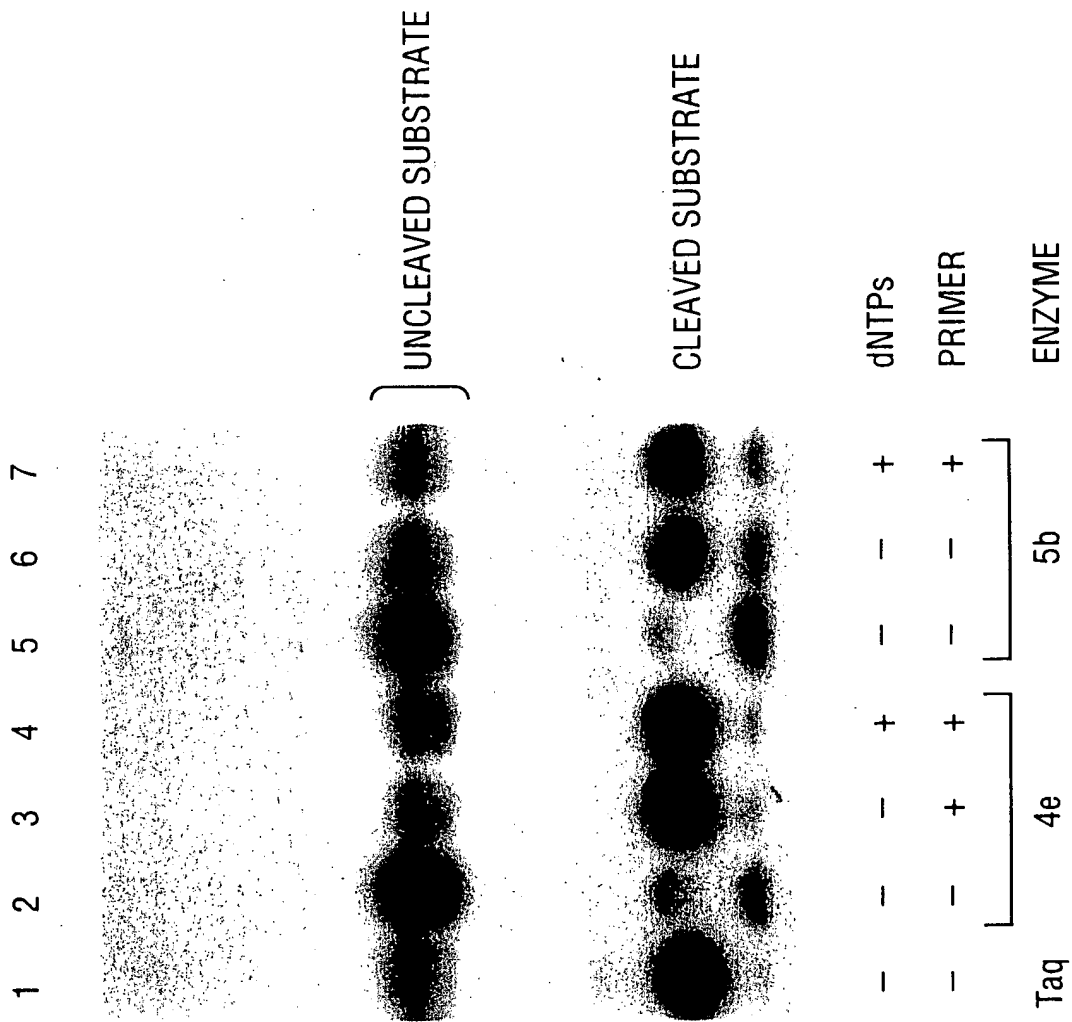


FIG. 16

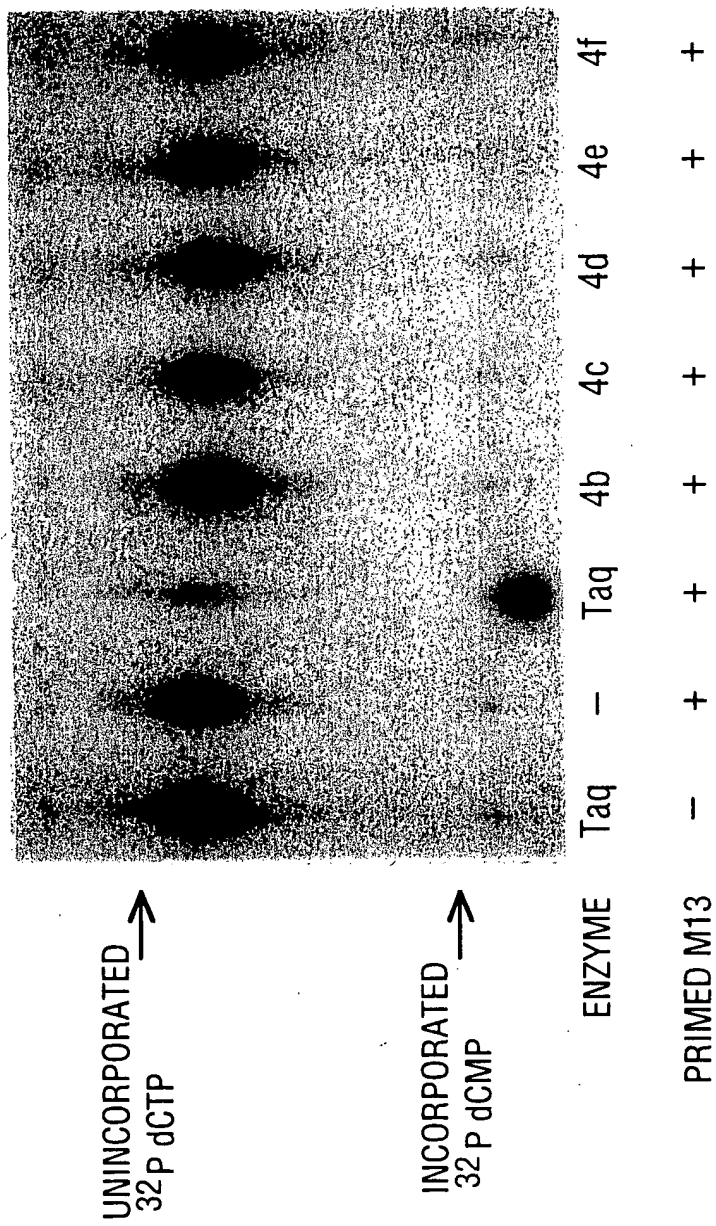
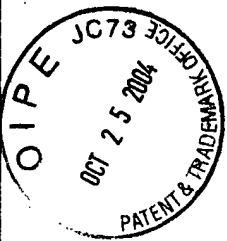


FIG. 17

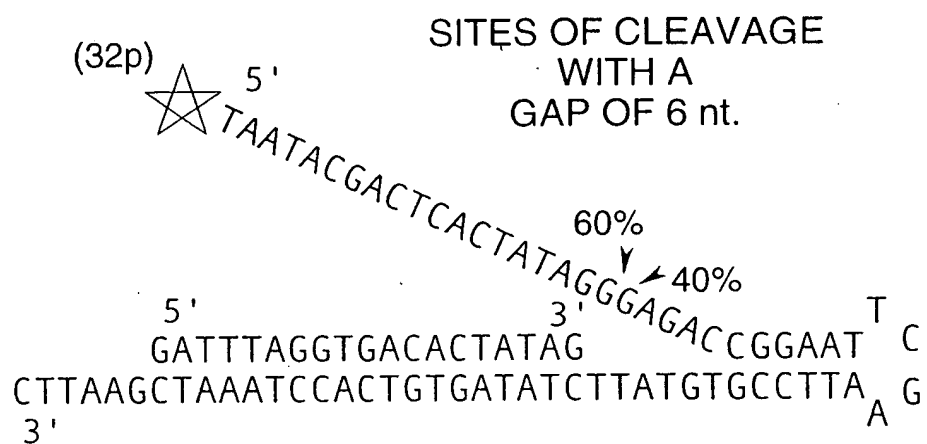
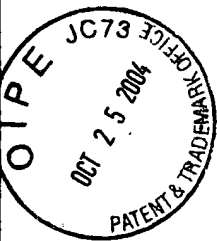


FIG. 18A

	"4d"	"4b"	UNMODIFIED
	NO POL. ACTIVITY	2 PT. MUTATION SMALL ACTIVITY	DNAP Taq
1	2	5	7
	3	6	8
	-	-	-
	+	+	+

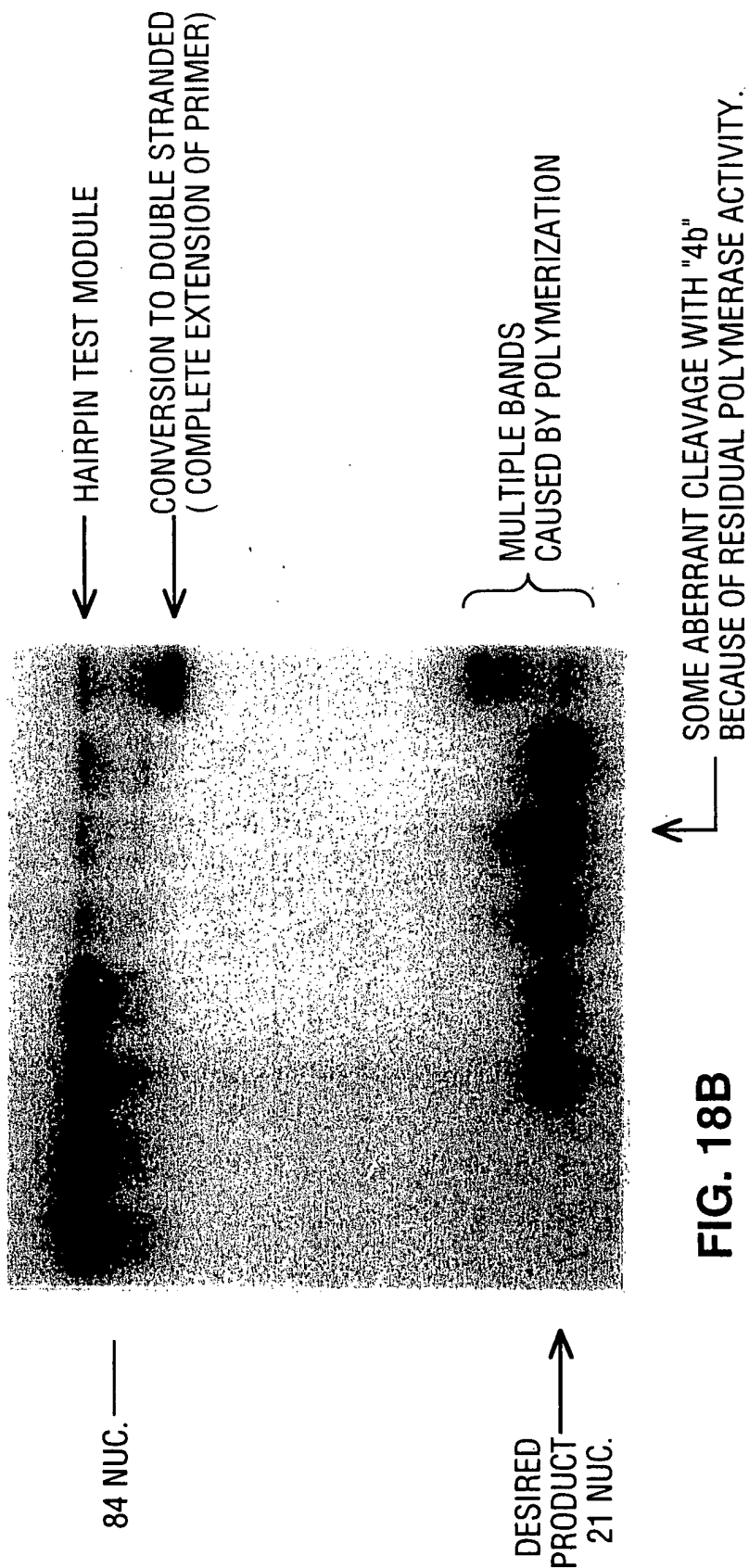


FIG. 18B

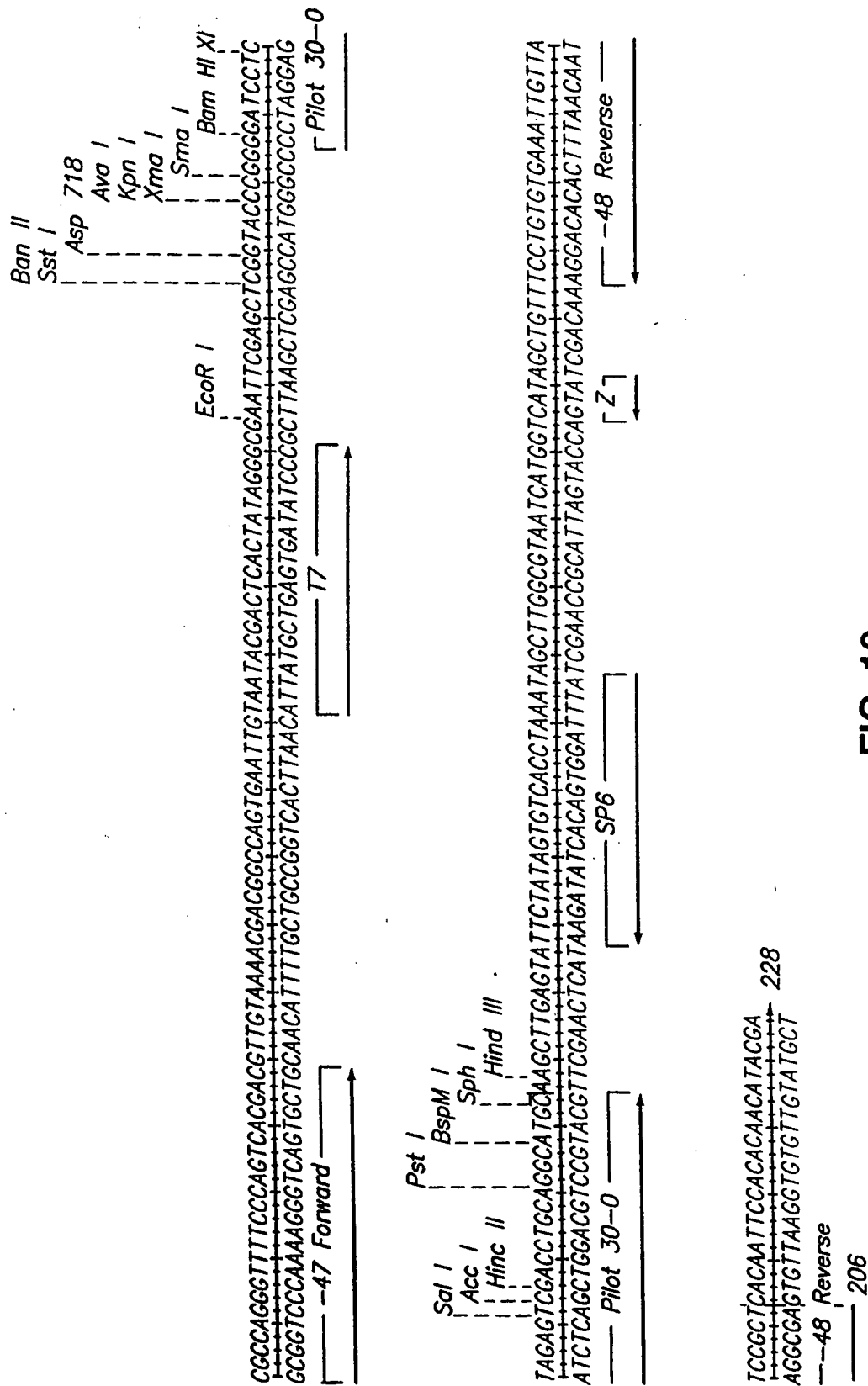


FIG. 19

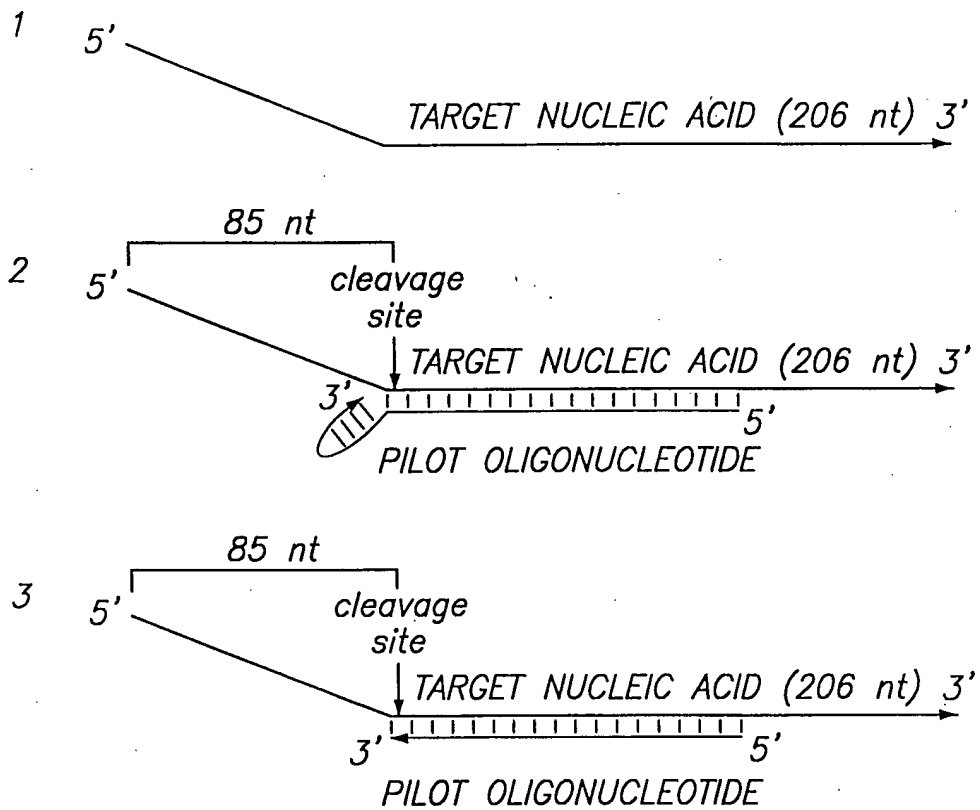


FIG. 20A

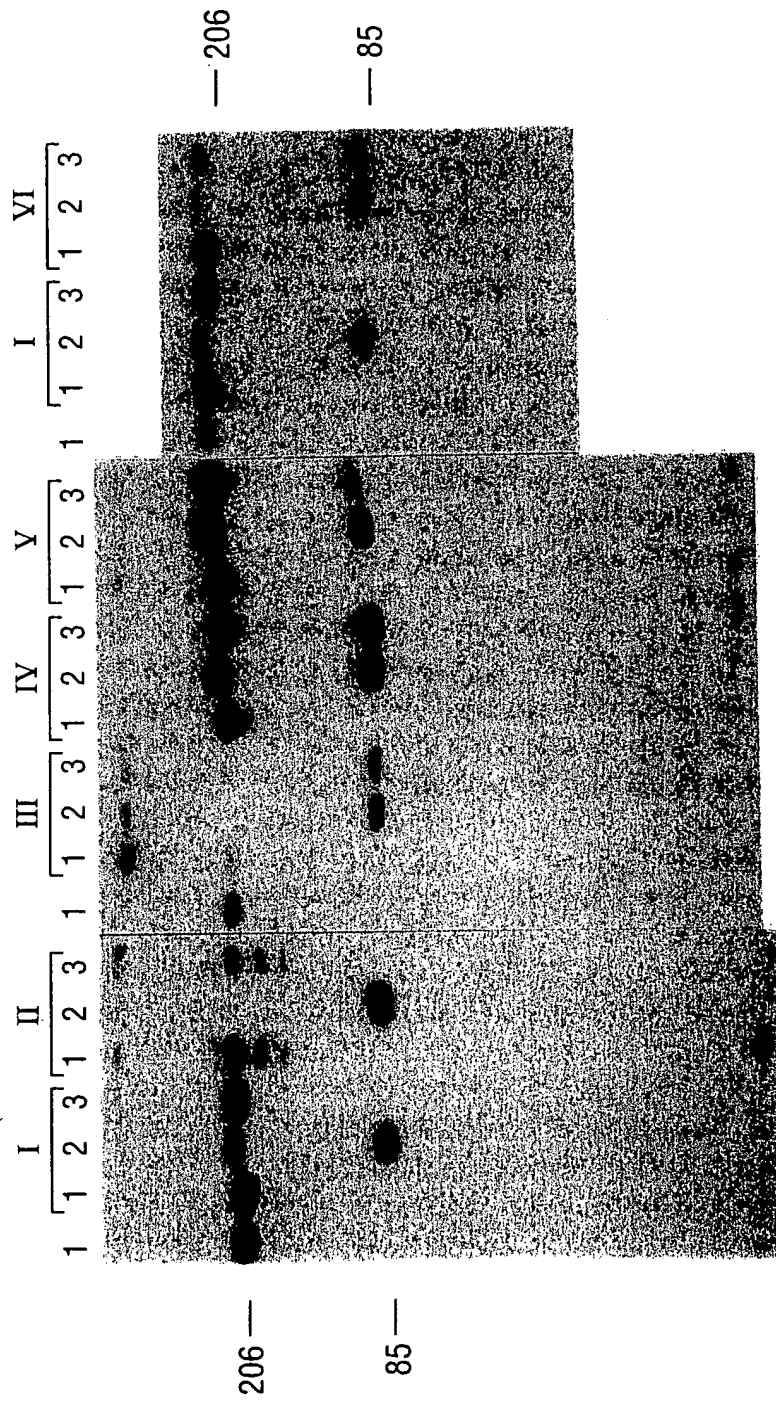


FIG. 20B

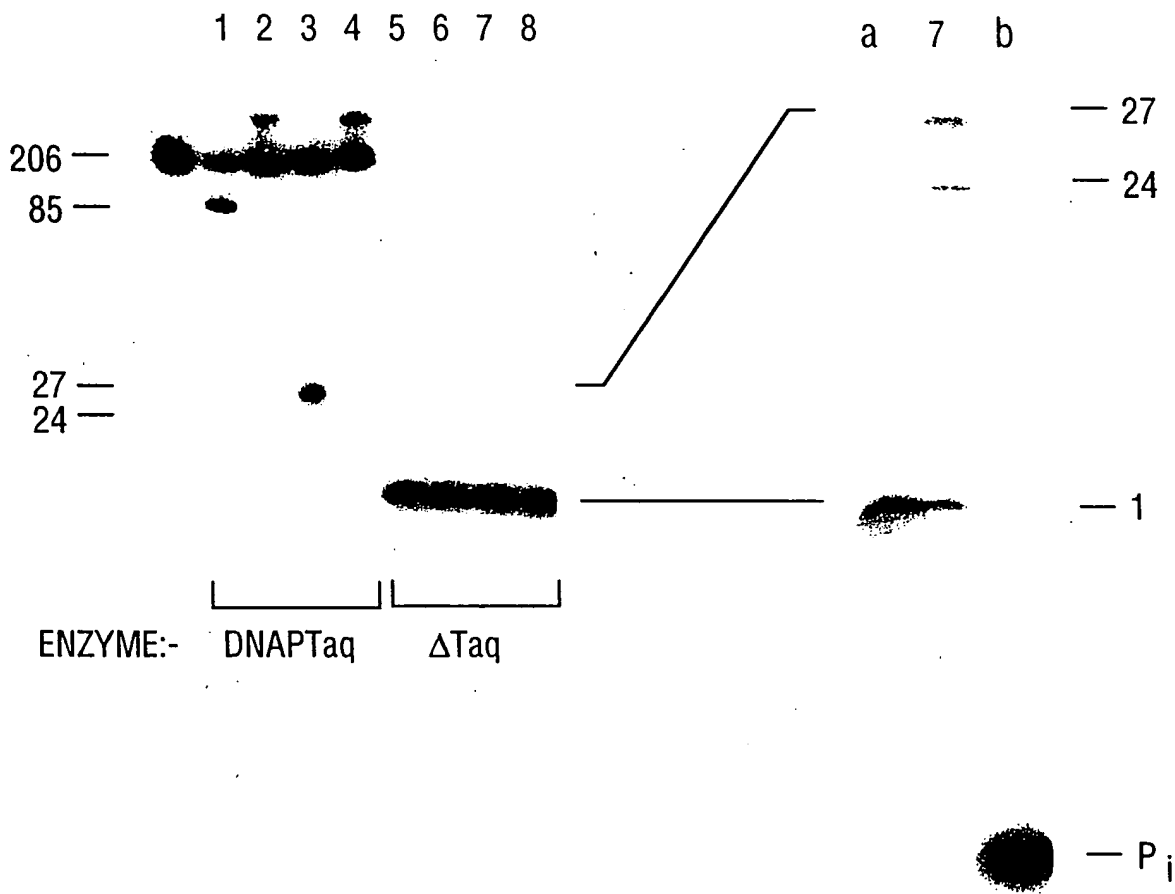
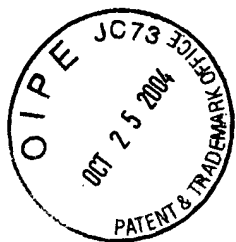


FIG. 21A

FIG. 21B

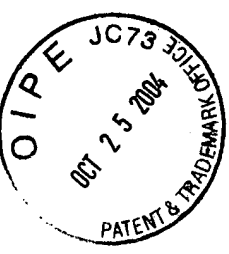


FIG. 22A



FIG. 22B

* = 32p



— 206

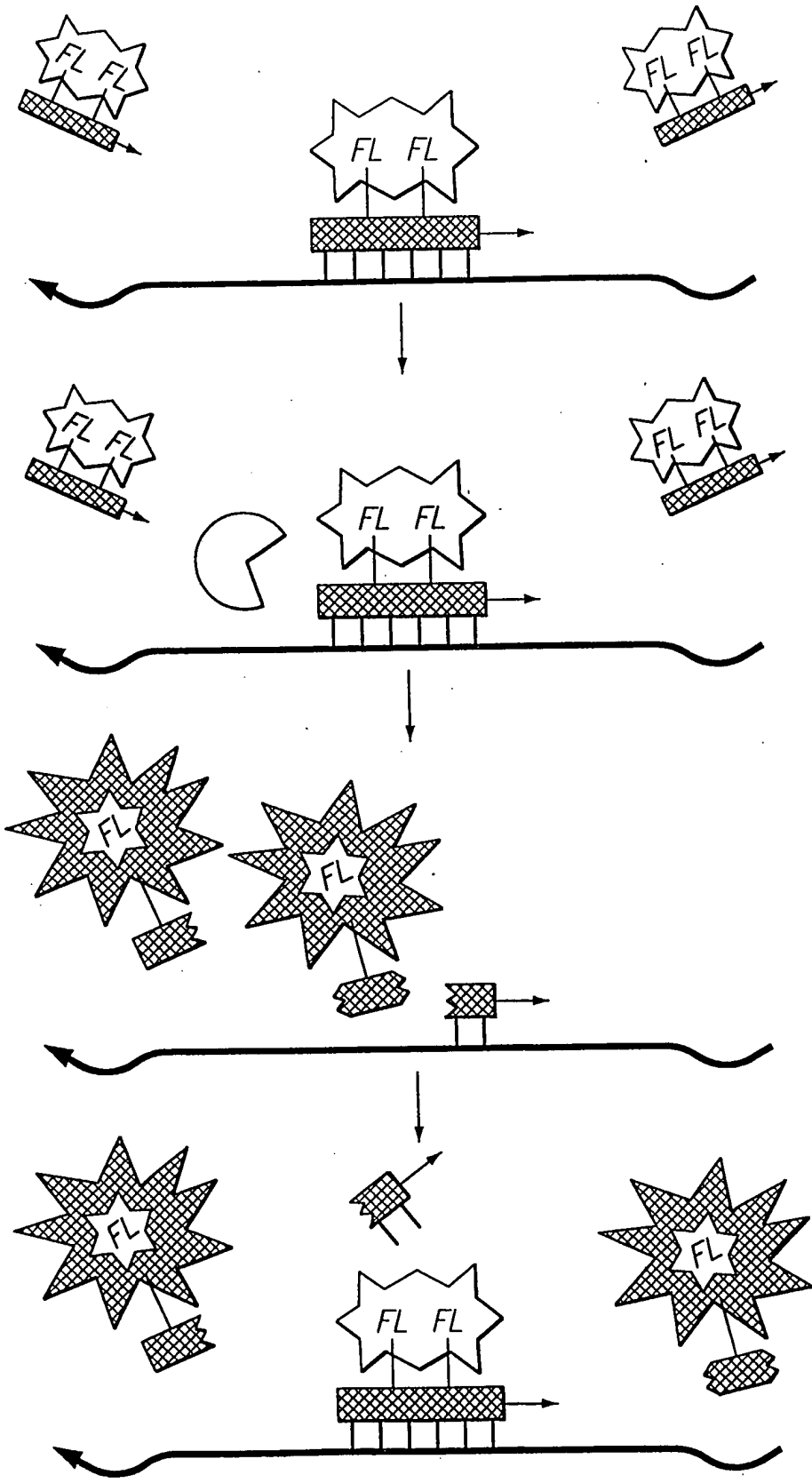
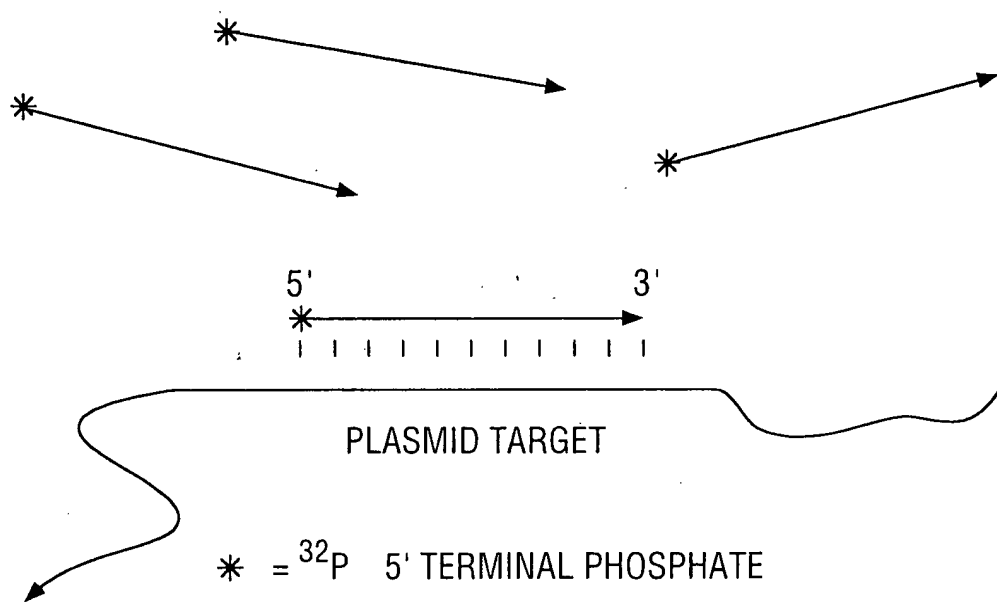


FIG. 23



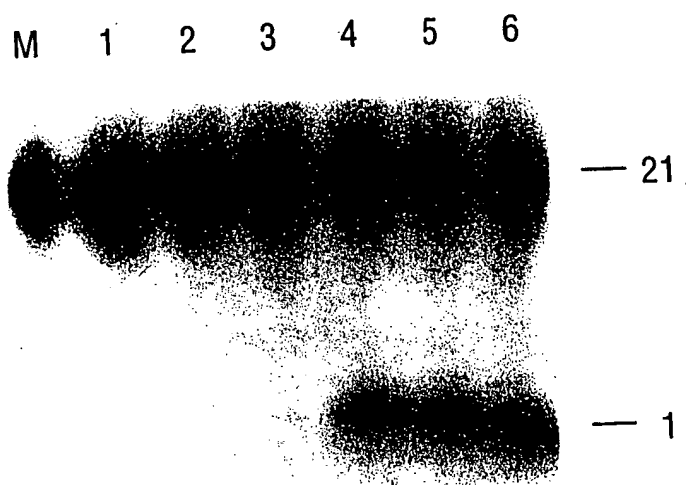
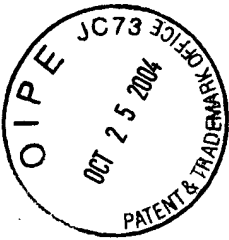


FIG. 24B

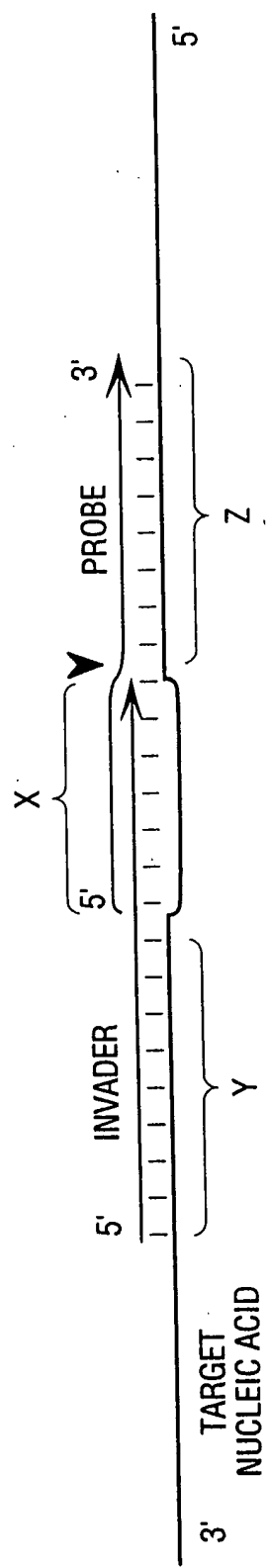
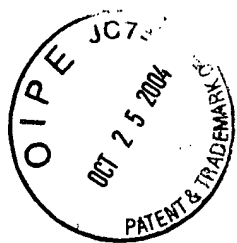


FIG. 25

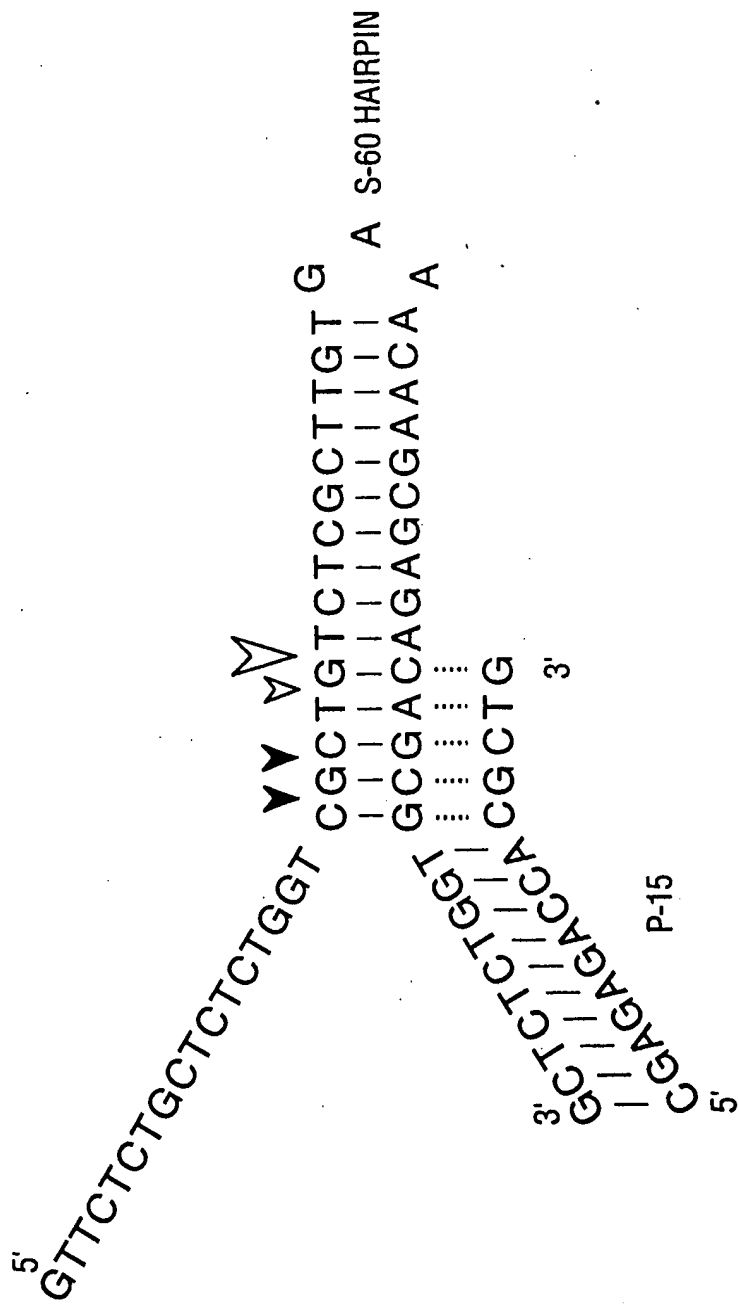
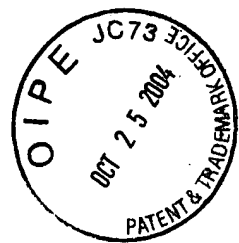


FIG. 26

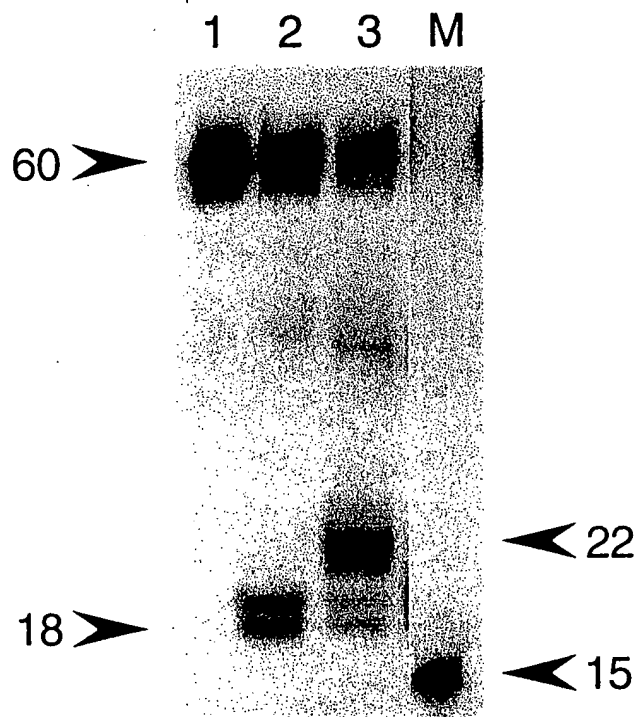
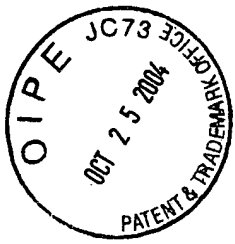


FIG. 27

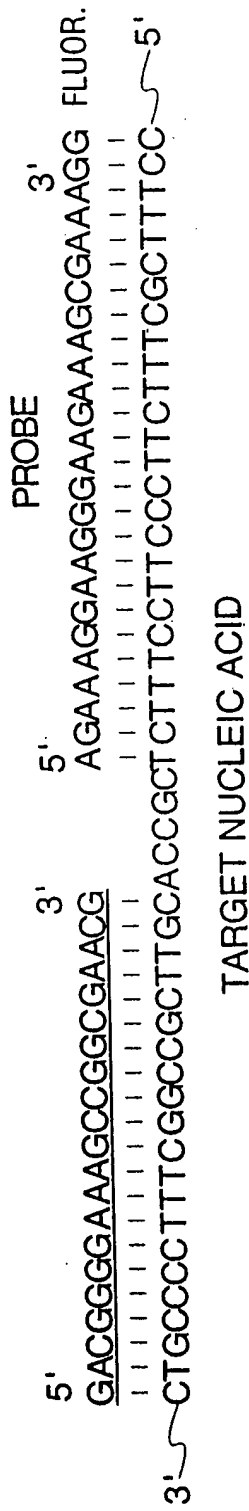
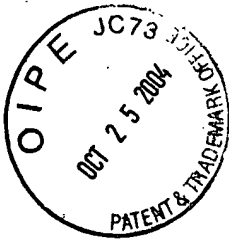


FIG. 28A

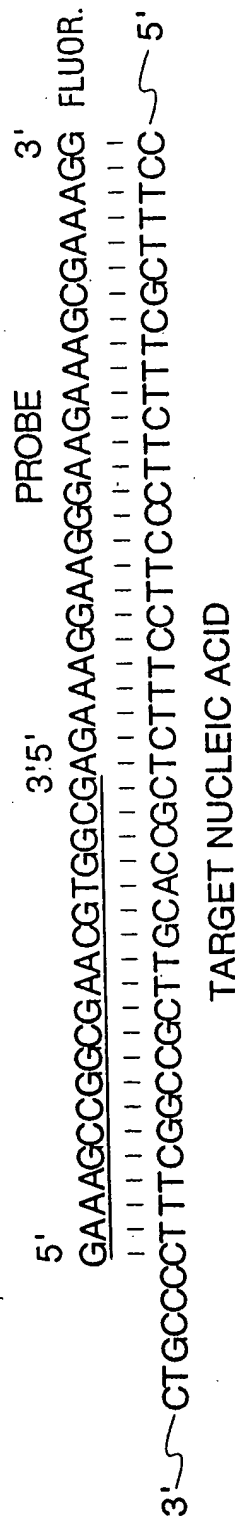


FIG. 28B

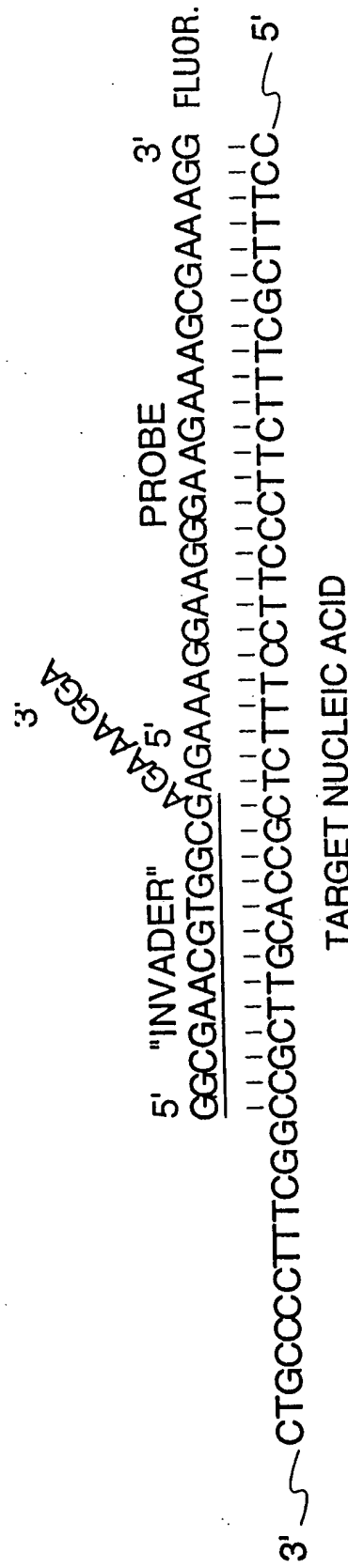


FIG. 28C

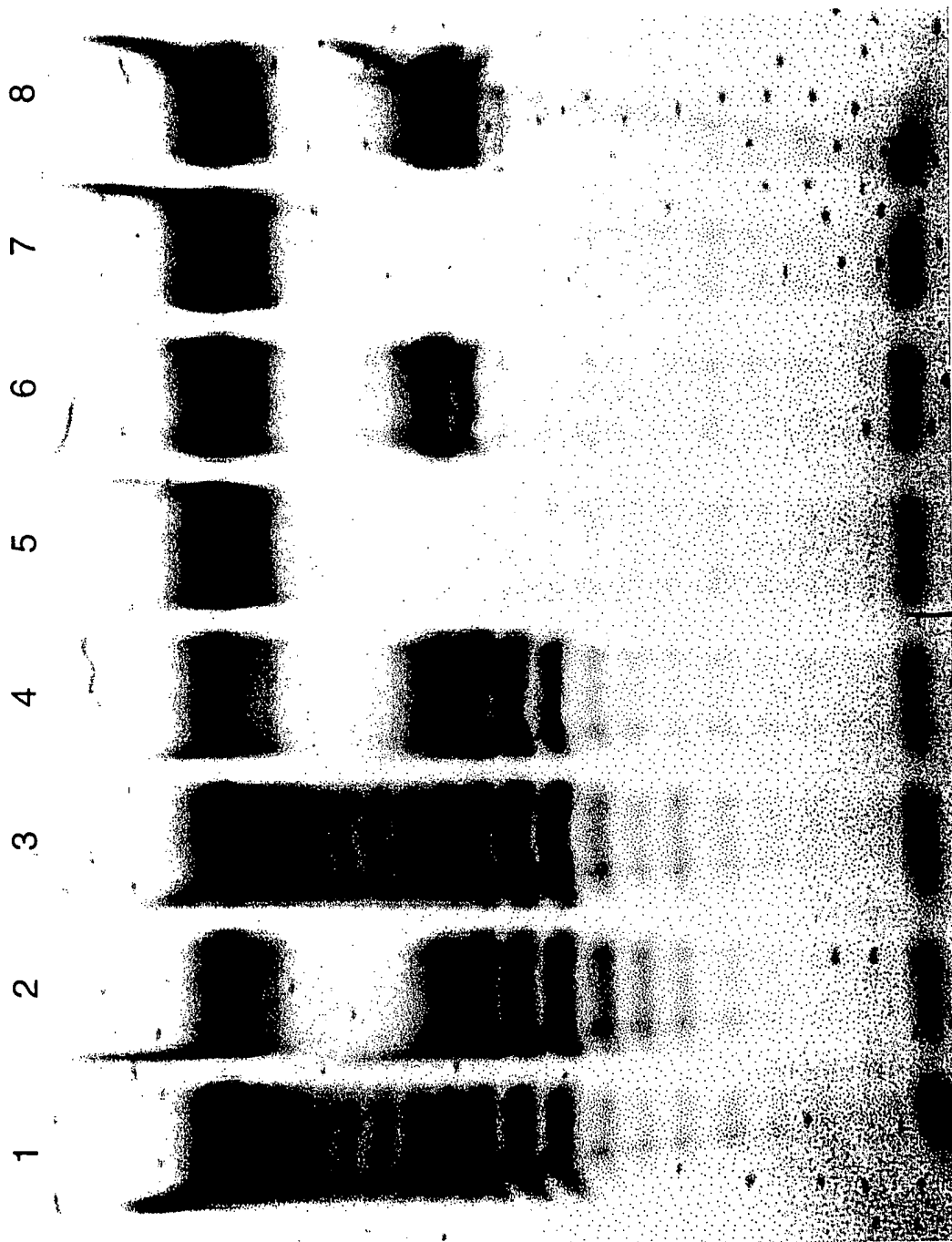
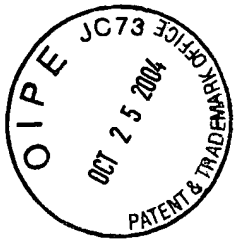


FIG. 29

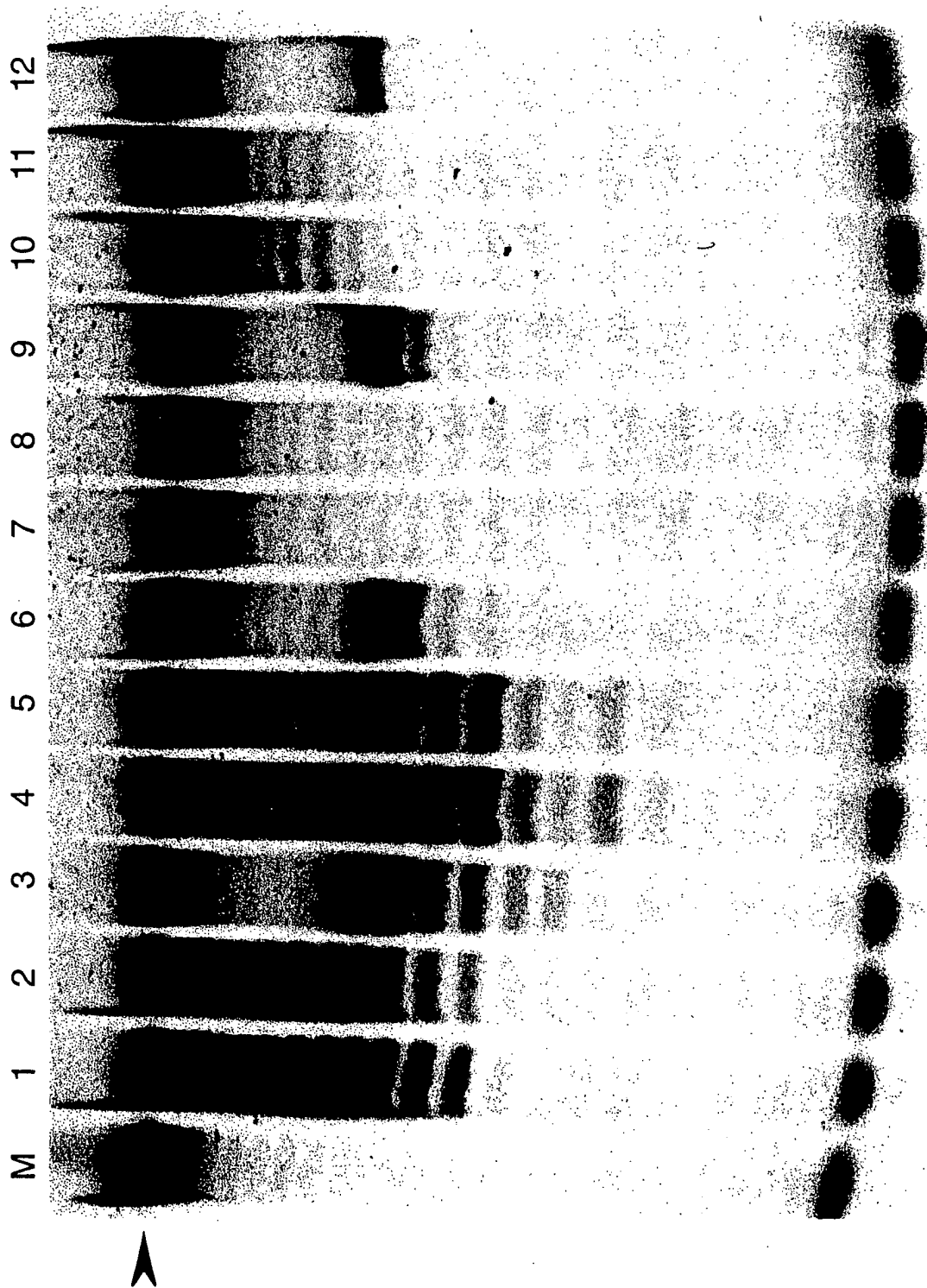
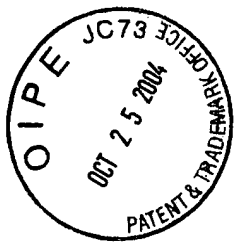


FIG. 30

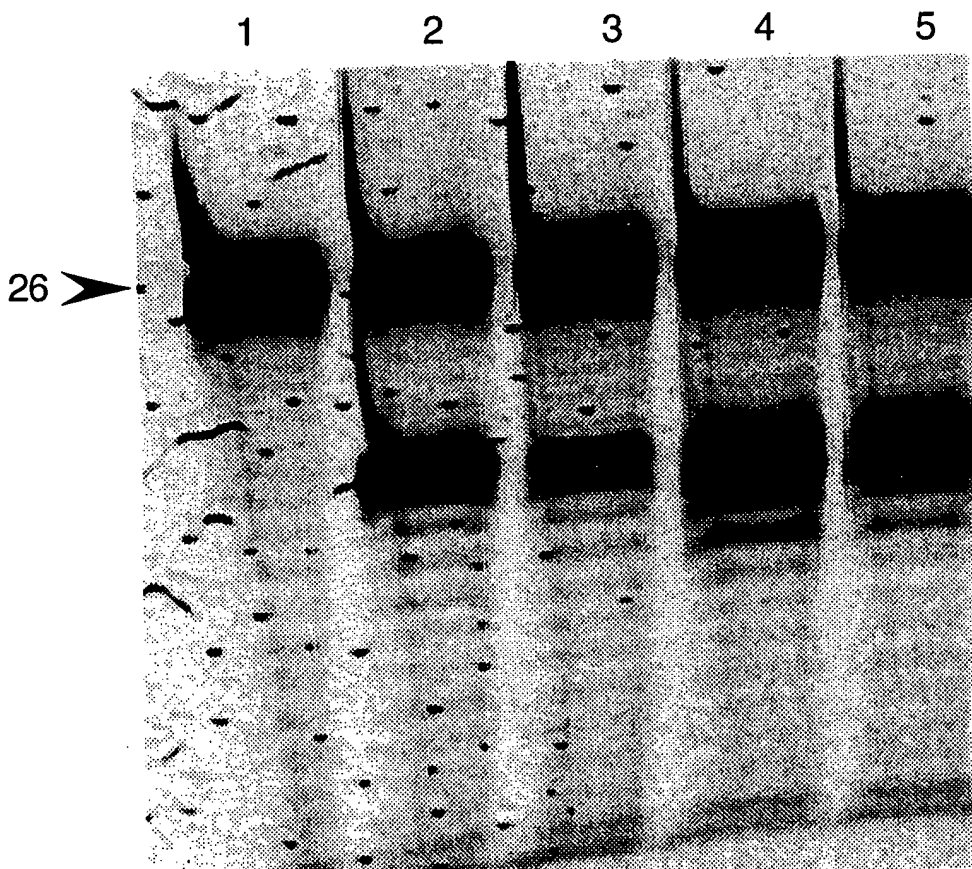


FIG. 31

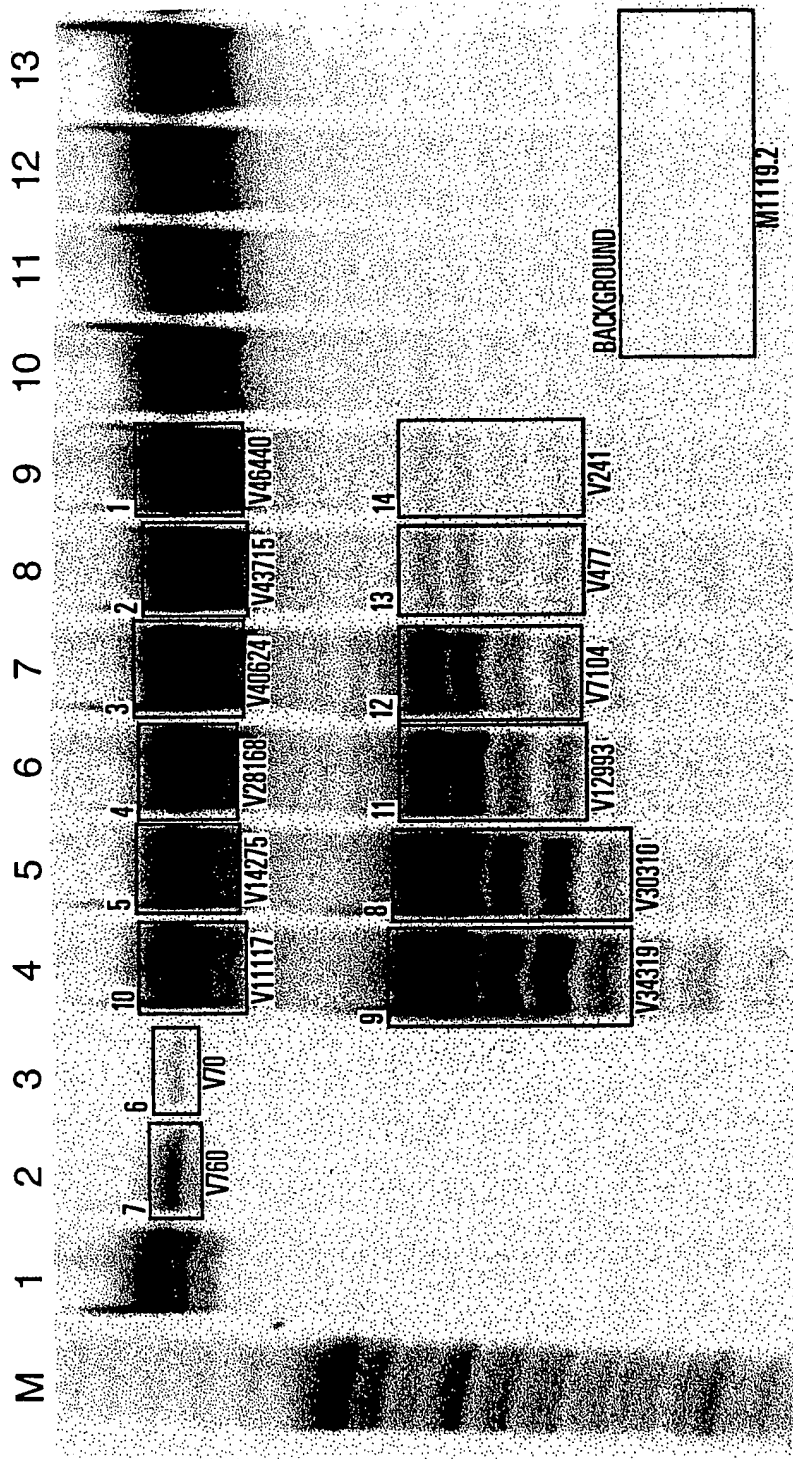


FIG. 32

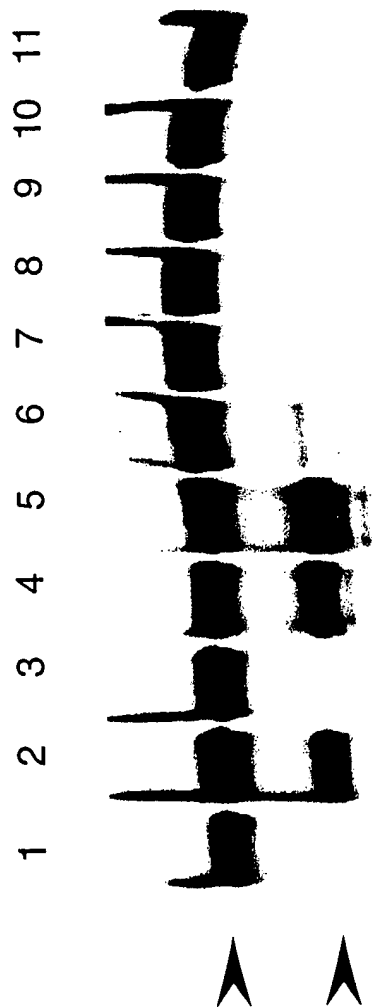
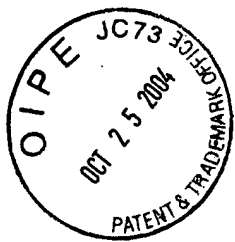


FIG. 33

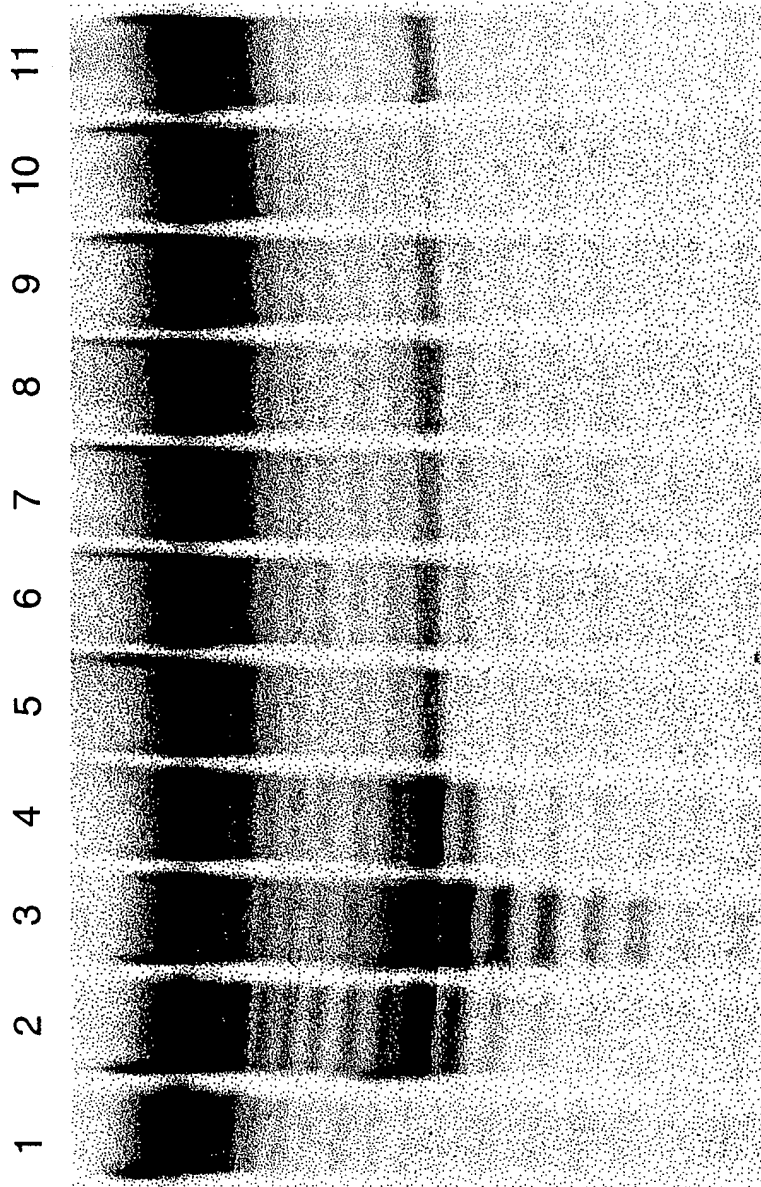
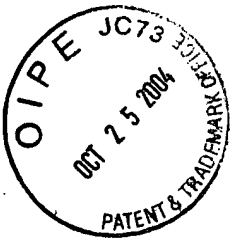


FIG. 34

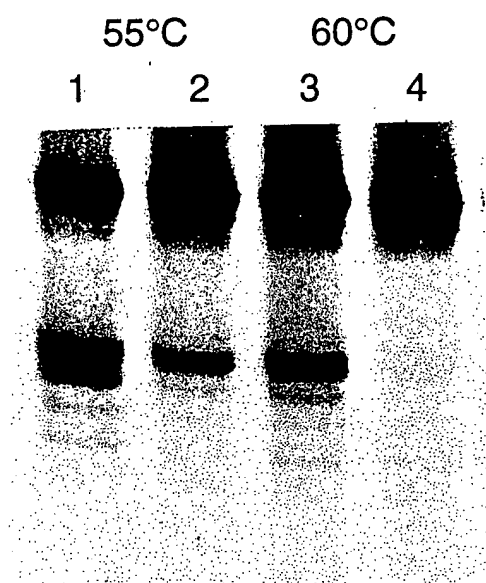
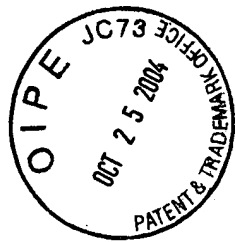


FIG. 35

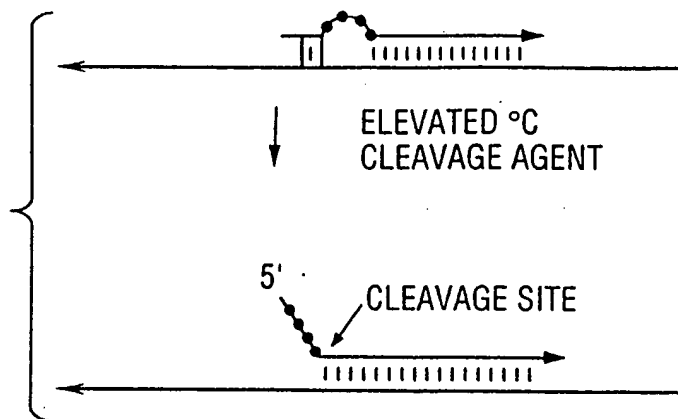


FIG. 36A

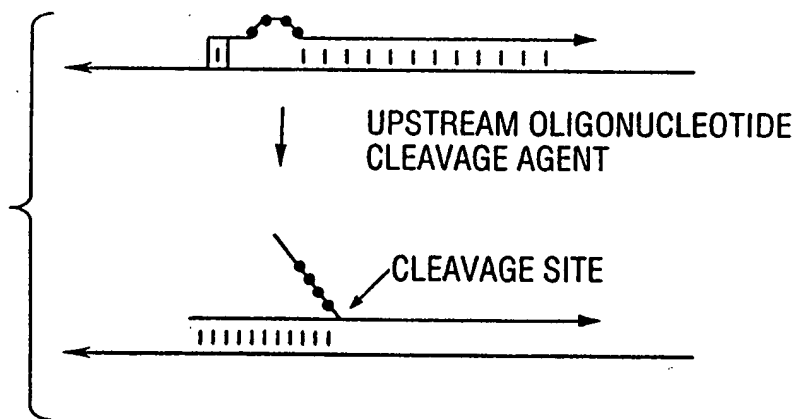


FIG. 36B

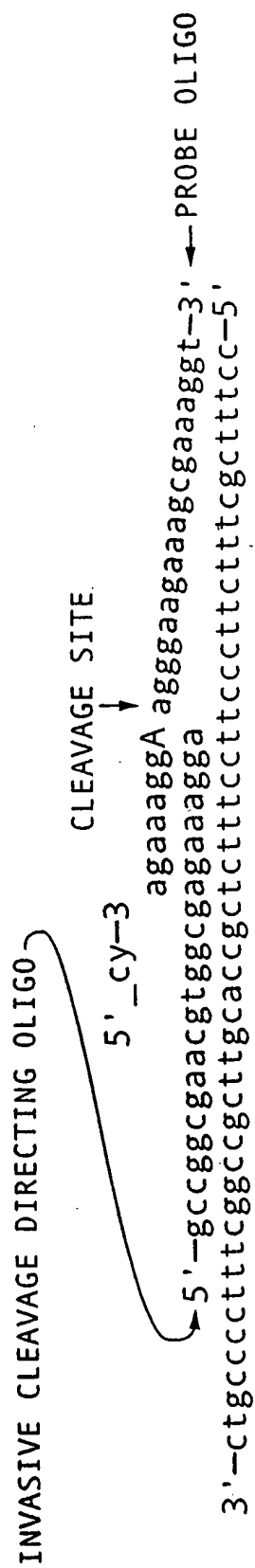
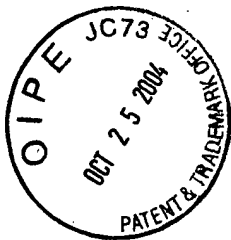


FIG. 37

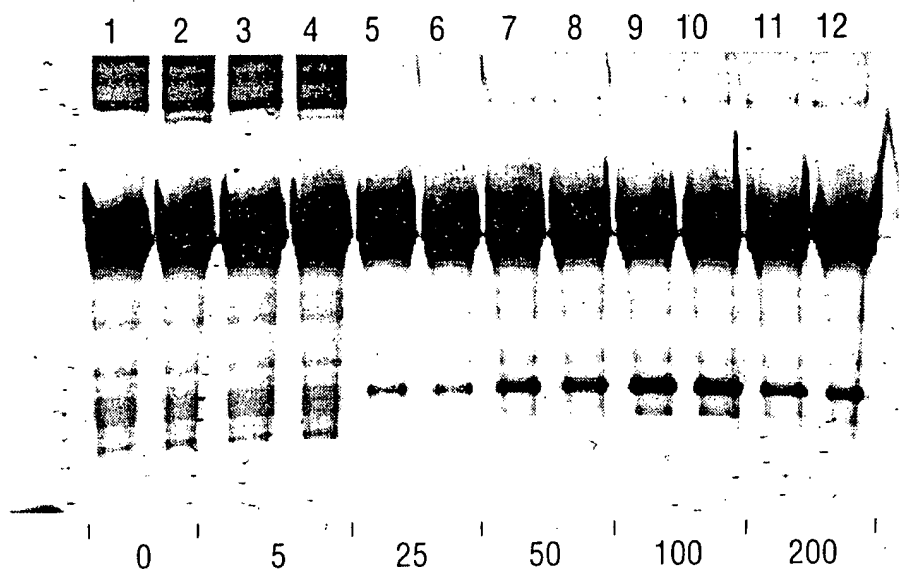
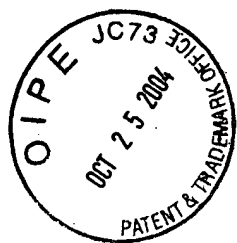


FIG. 38

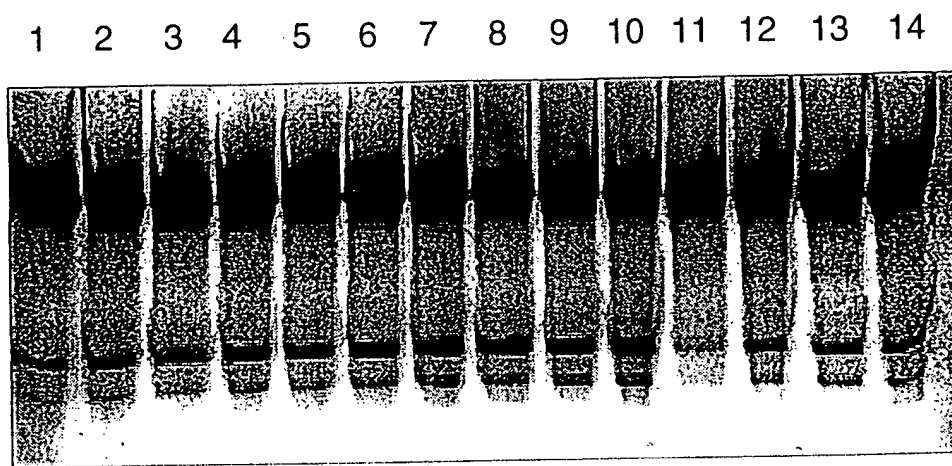
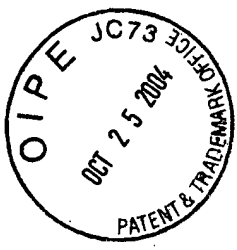


FIG. 39

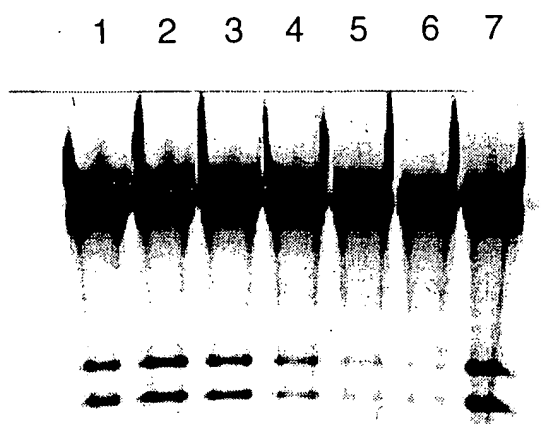
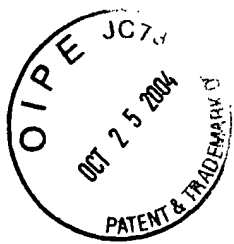


FIG. 40

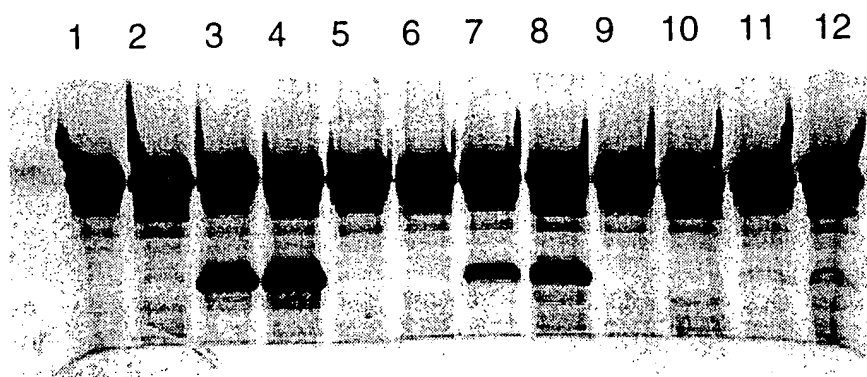
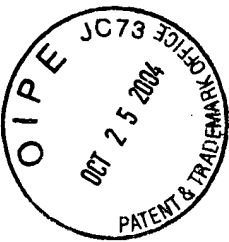


FIG. 41

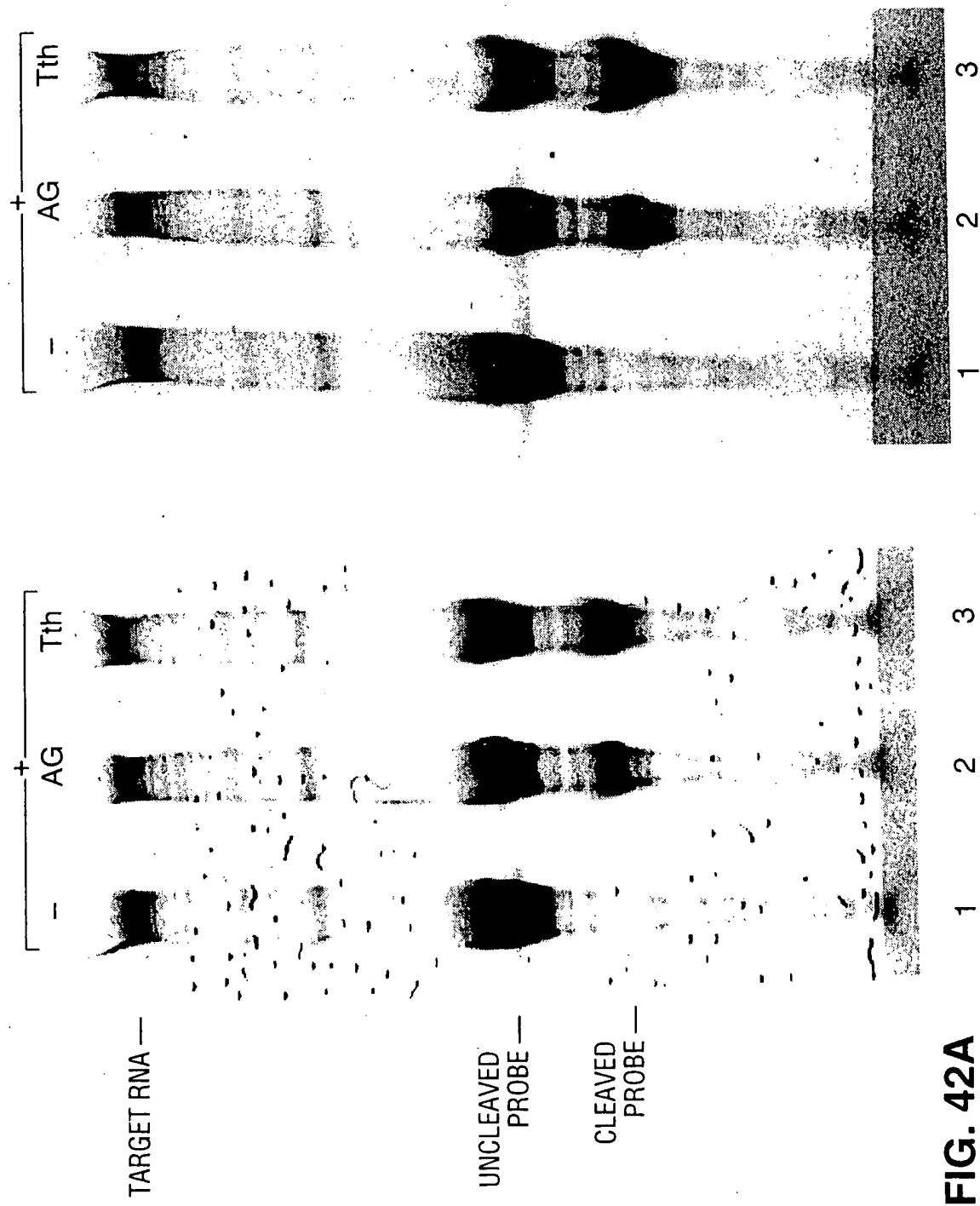


FIG. 42B

FIG. 42A

— ENZYME
— TARGET (fmol)
— RNA

500 1 5 10 50 100 100 1 5 10 50 100

CLEAVASE AG

Tth

— PROBE

— PRODUCT

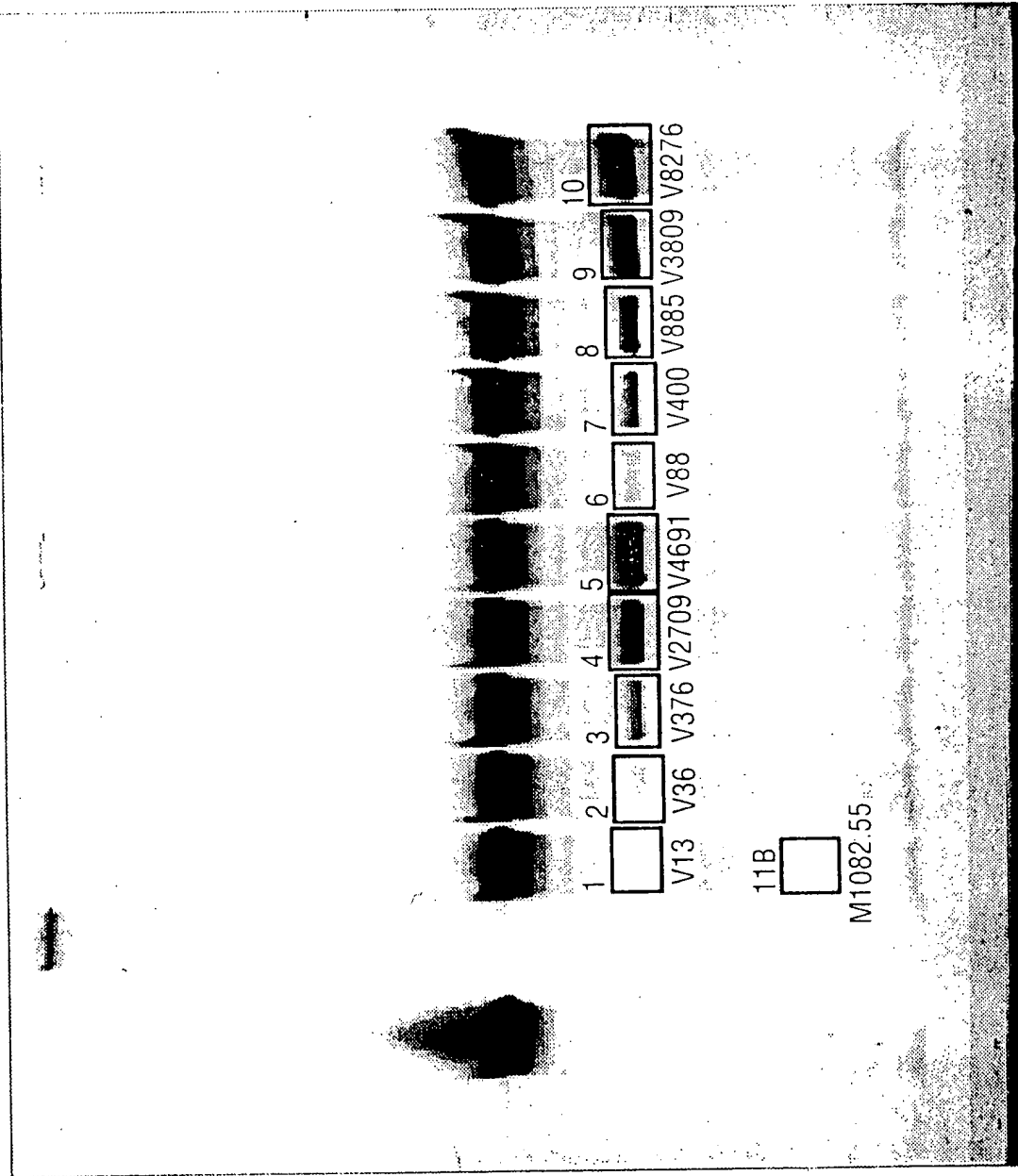


FIG. 43

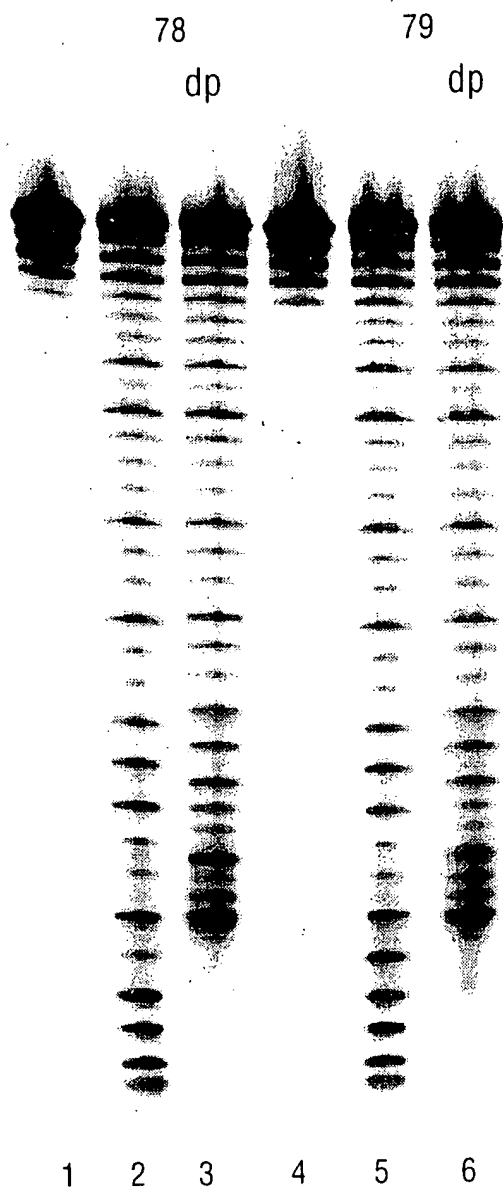
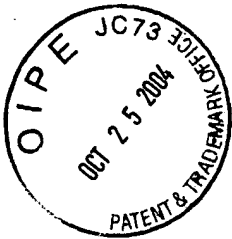


FIG. 44

70 (C10 amino T's)
74 (C6 amino T's)

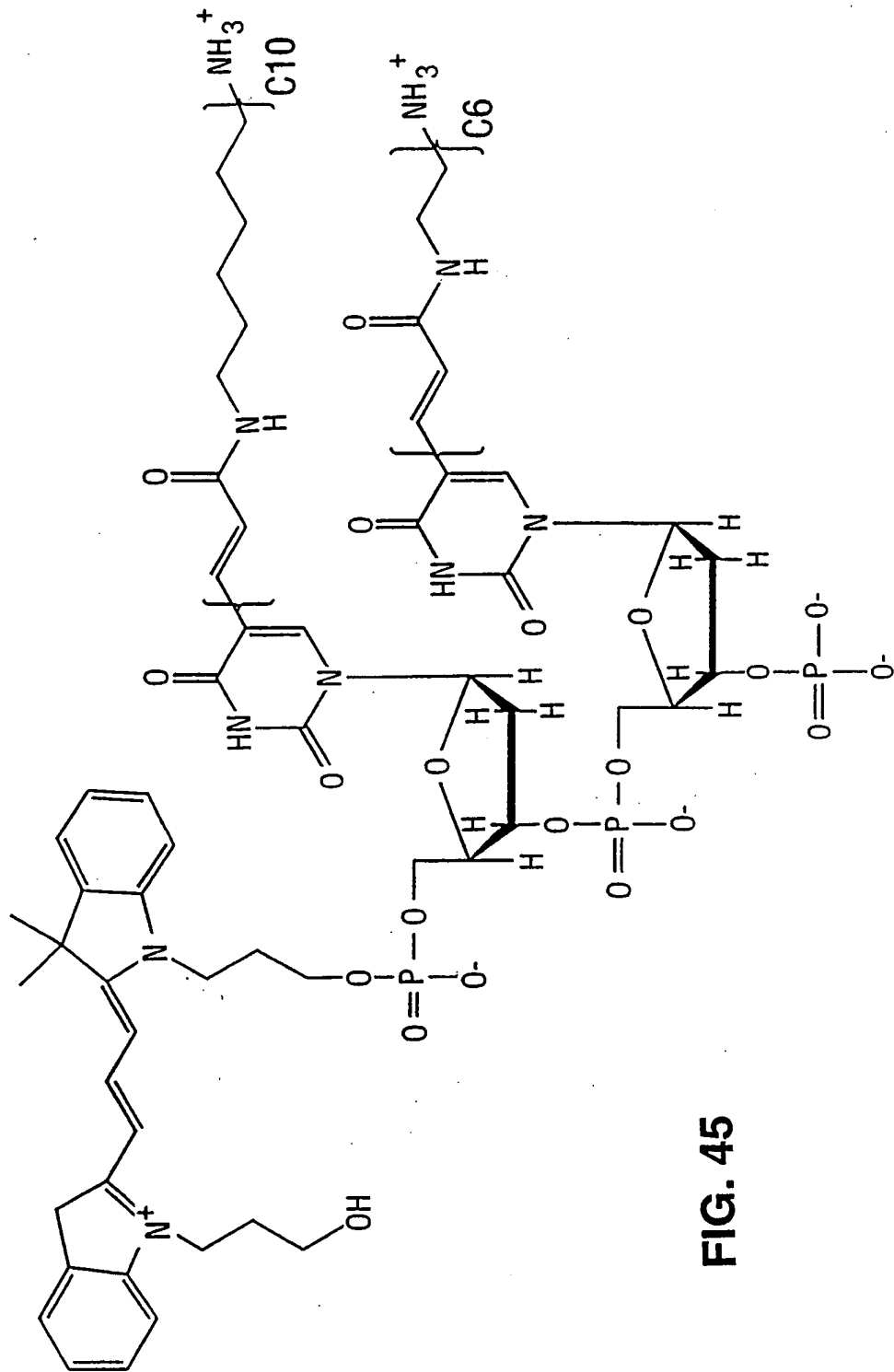


FIG. 45

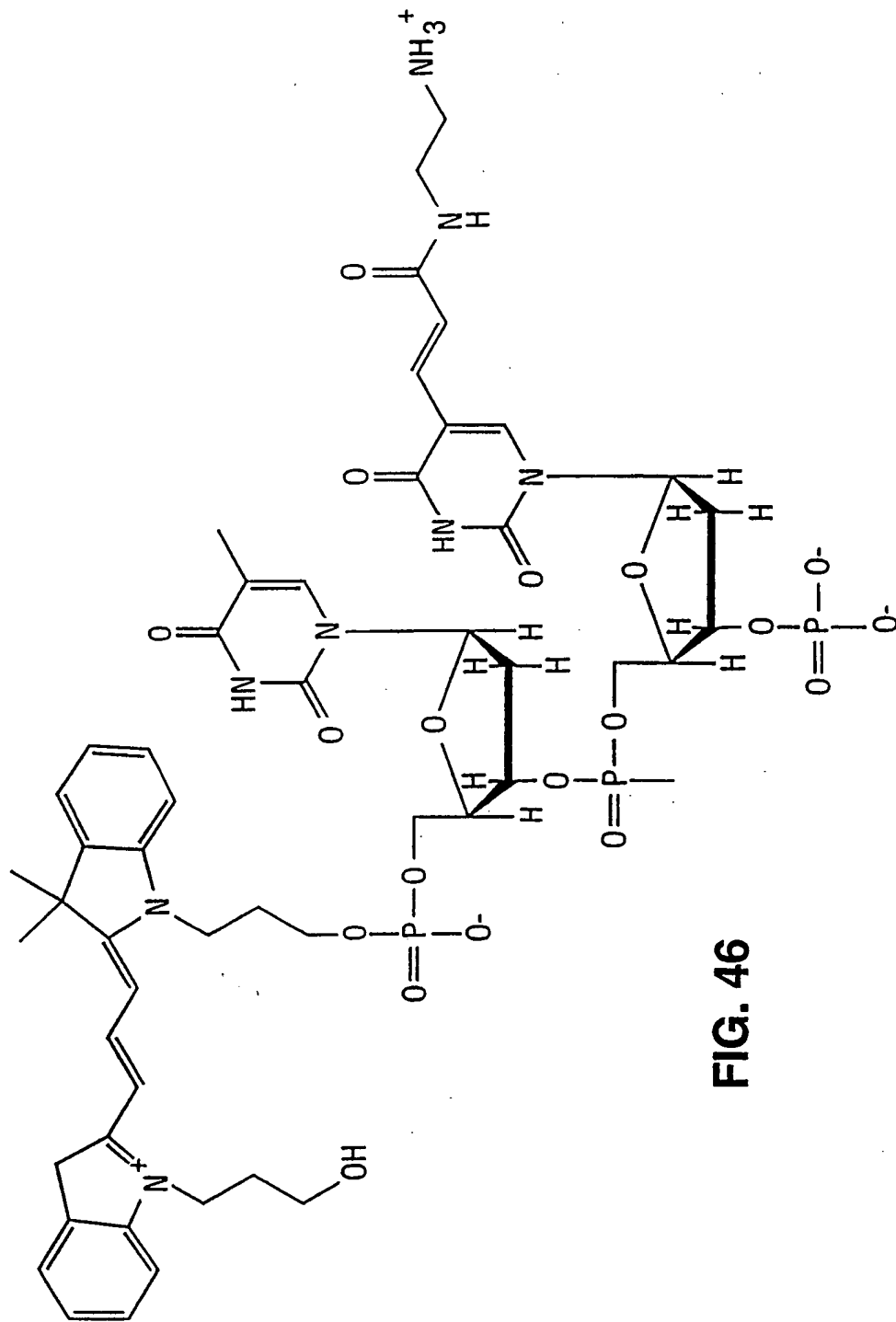


FIG. 46

FIG. 47

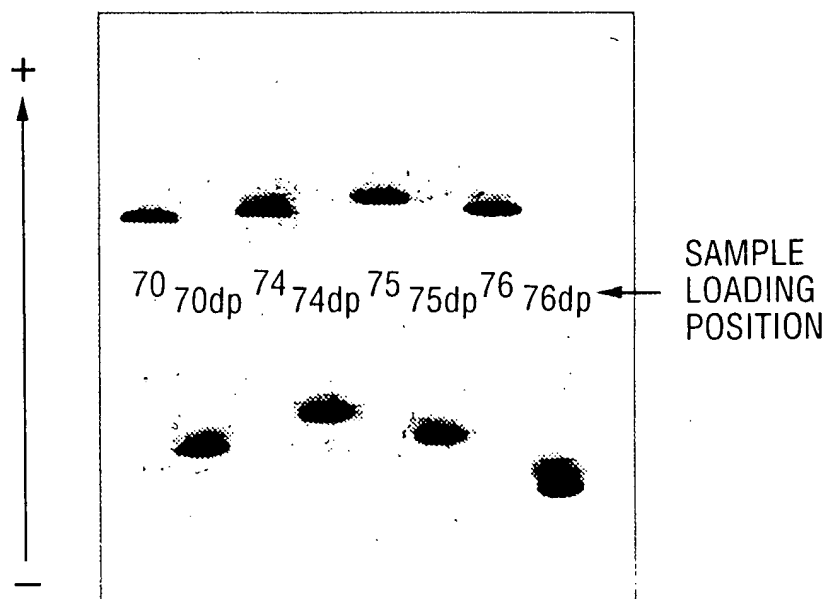


FIG. 48

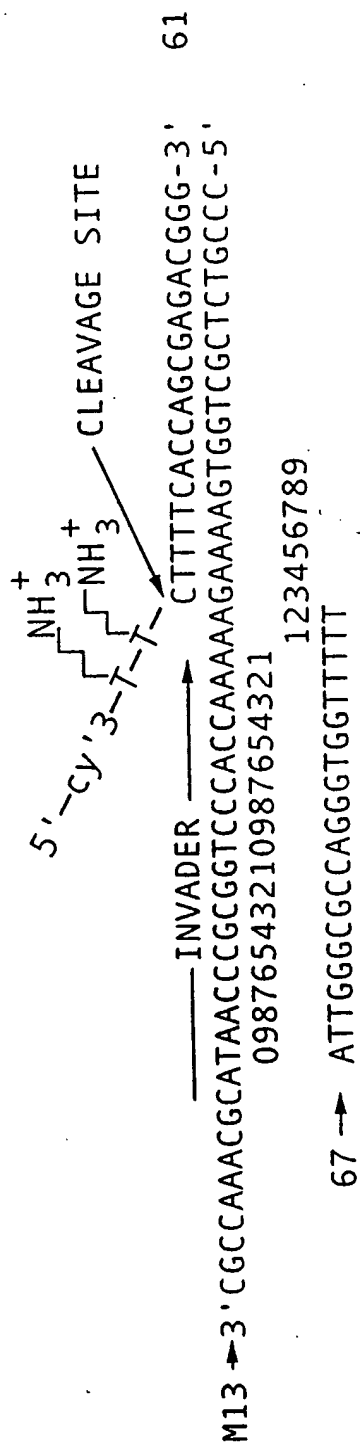


FIG. 49A

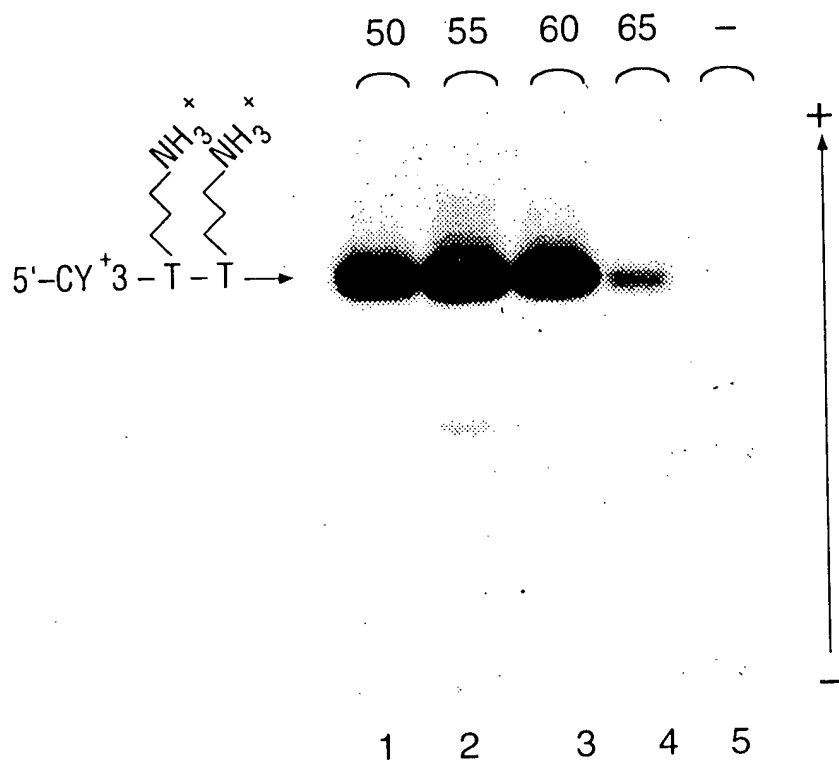


FIG. 49B

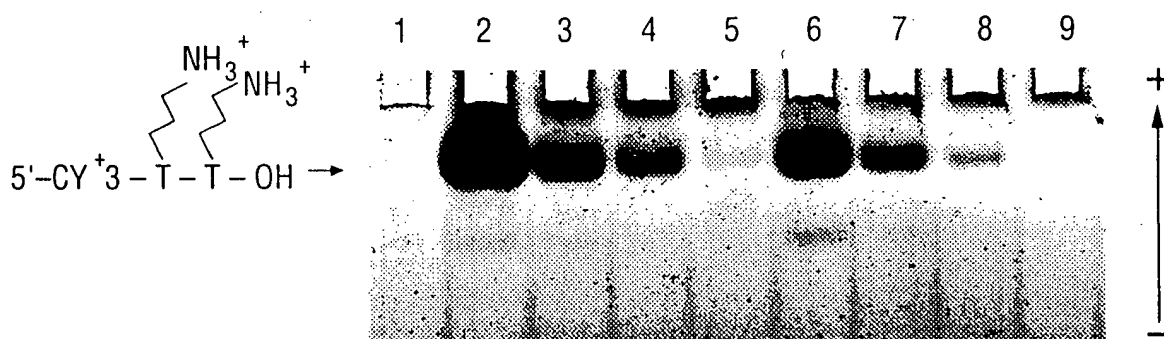
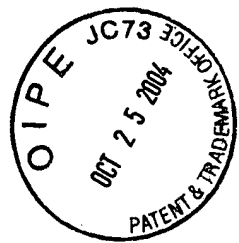


FIG. 50

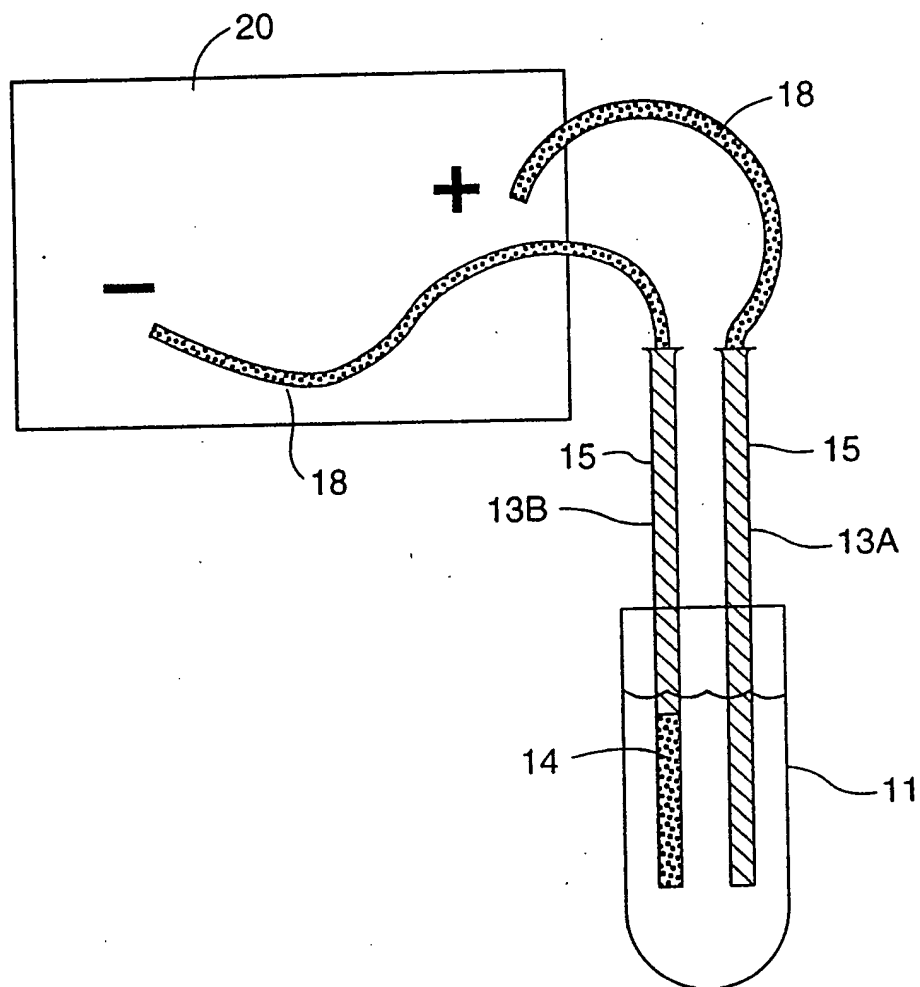
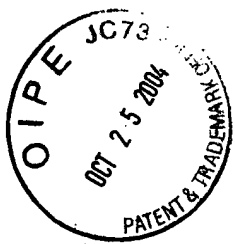


FIG. 51

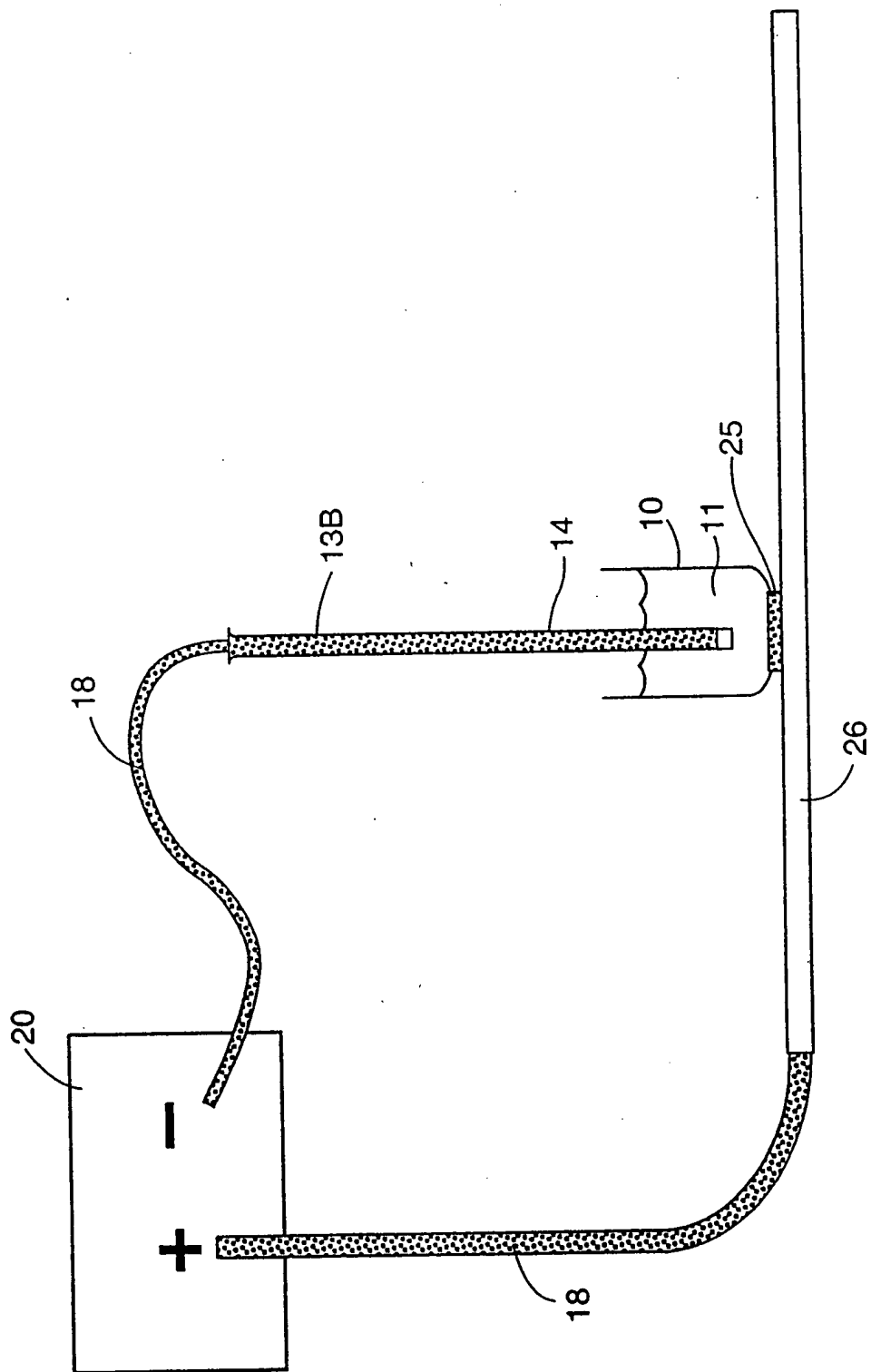


FIG. 52

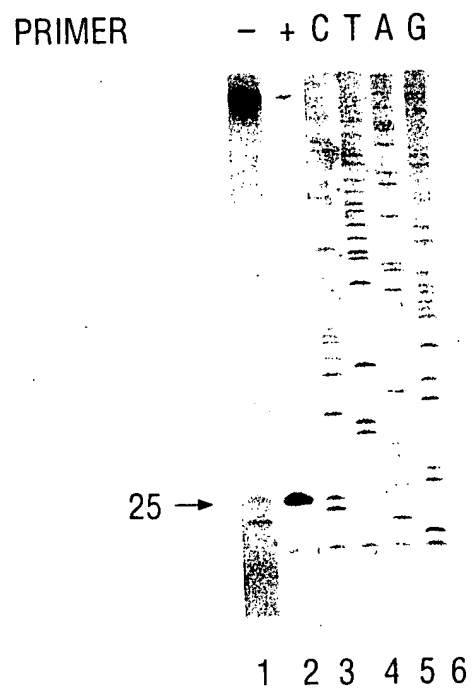
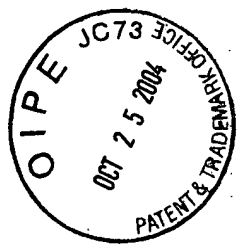


FIG. 53

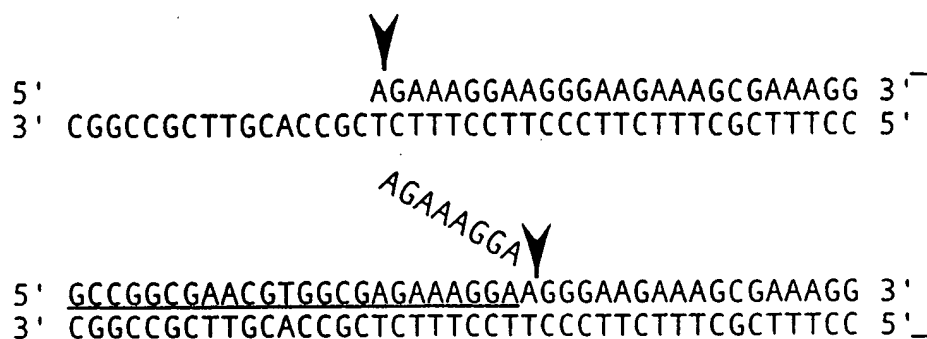


FIG. 54A

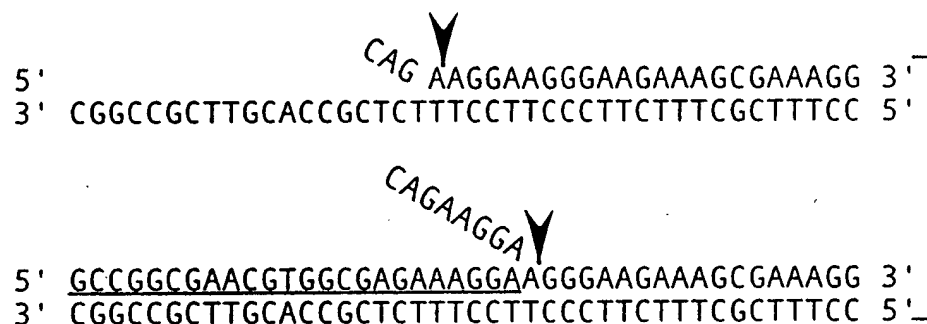


FIG. 54B

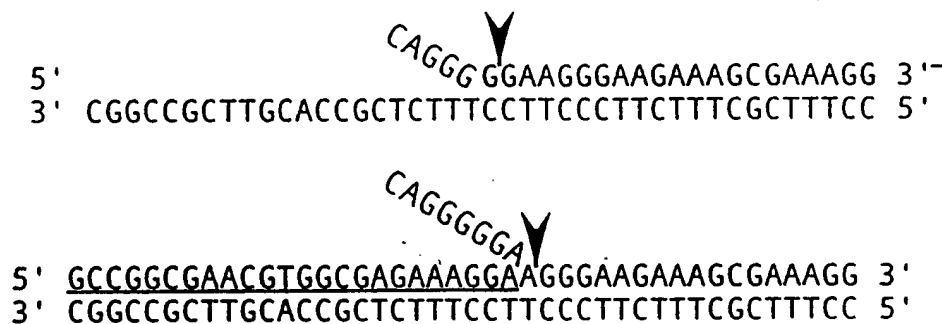


FIG. 54C



FIG. 54D

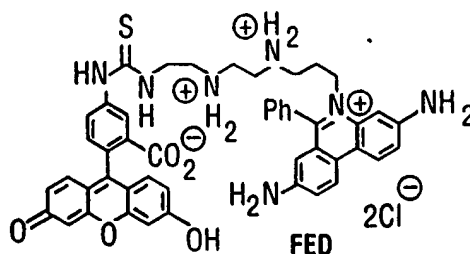
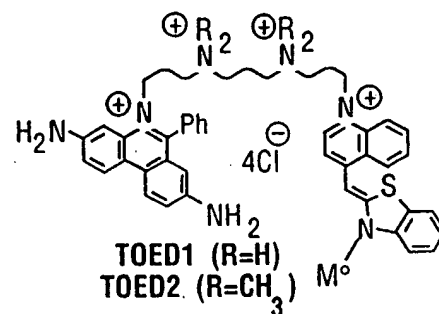
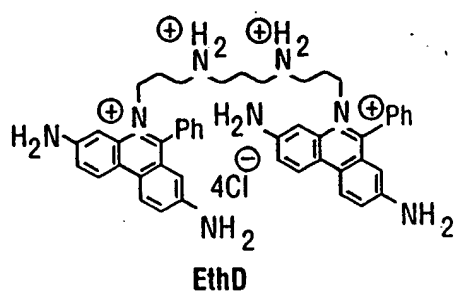
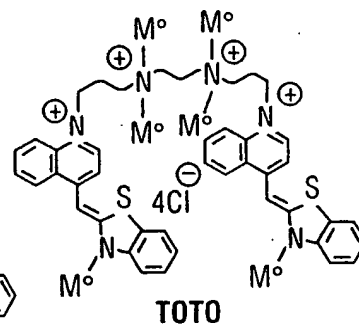
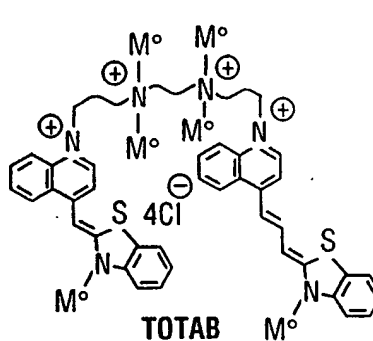
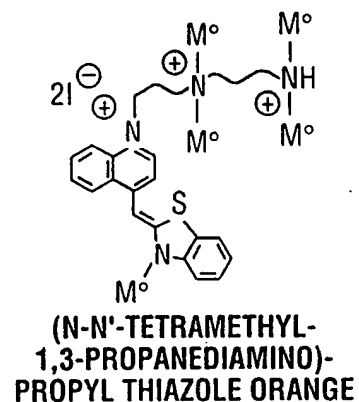
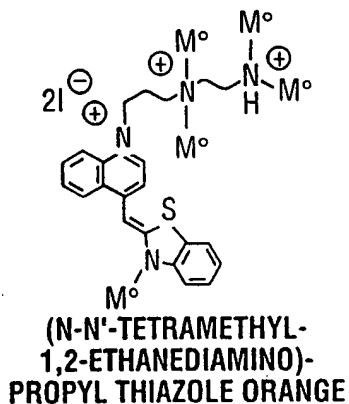
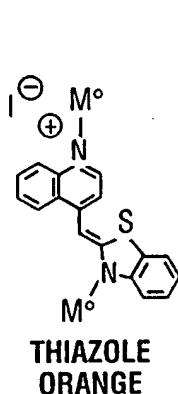
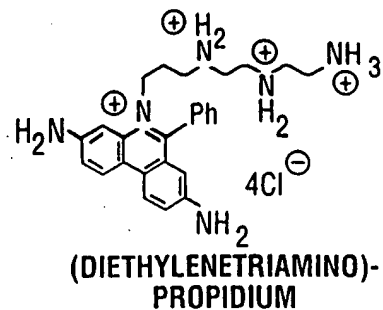
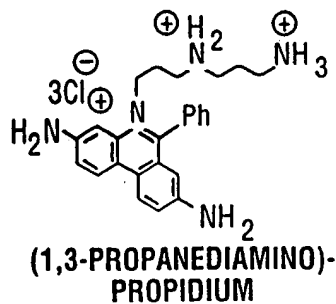
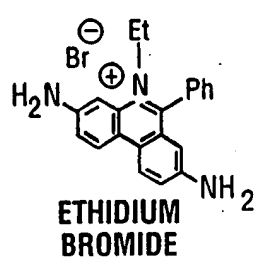


FIG. 55

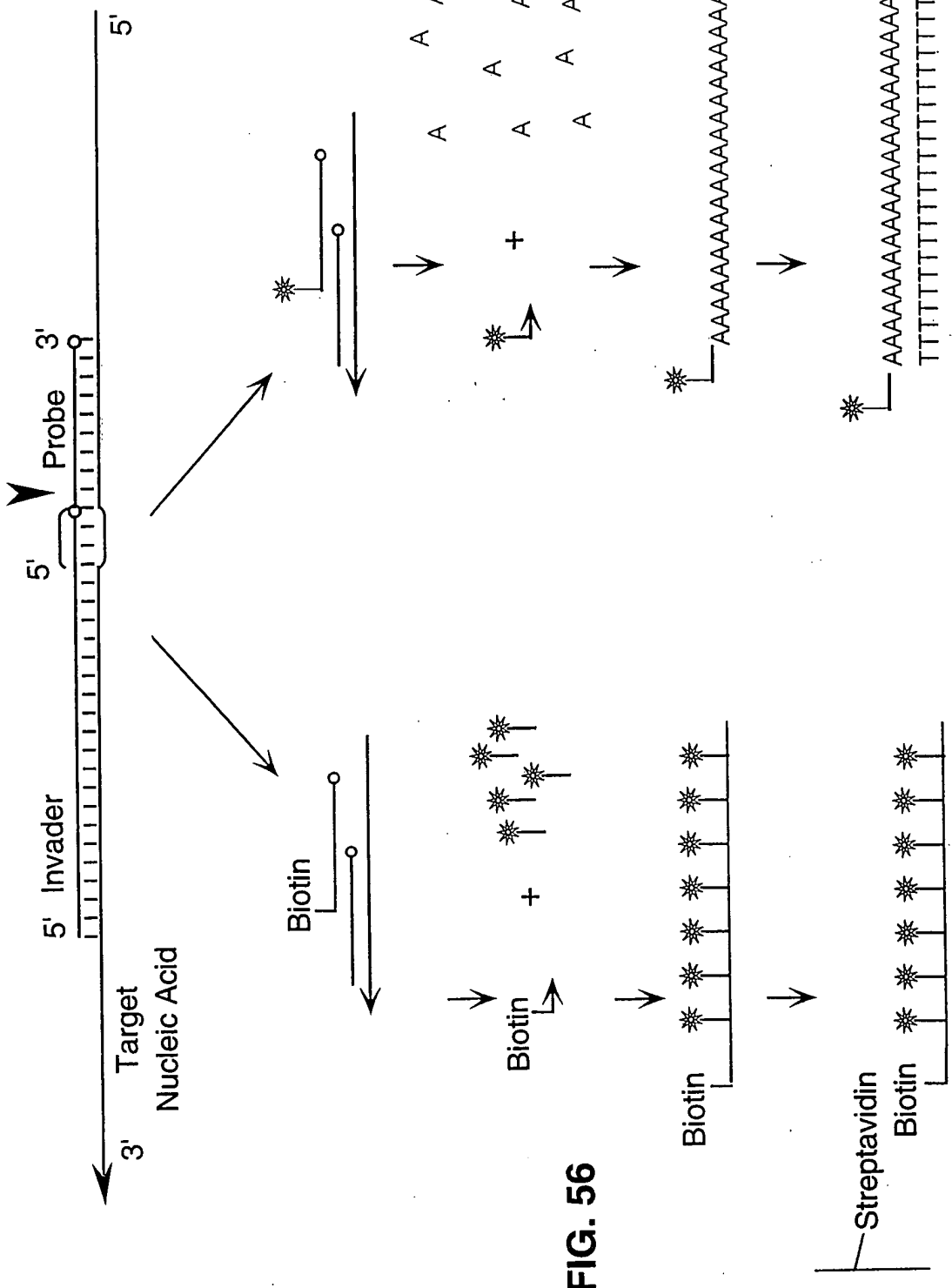


FIG. 56

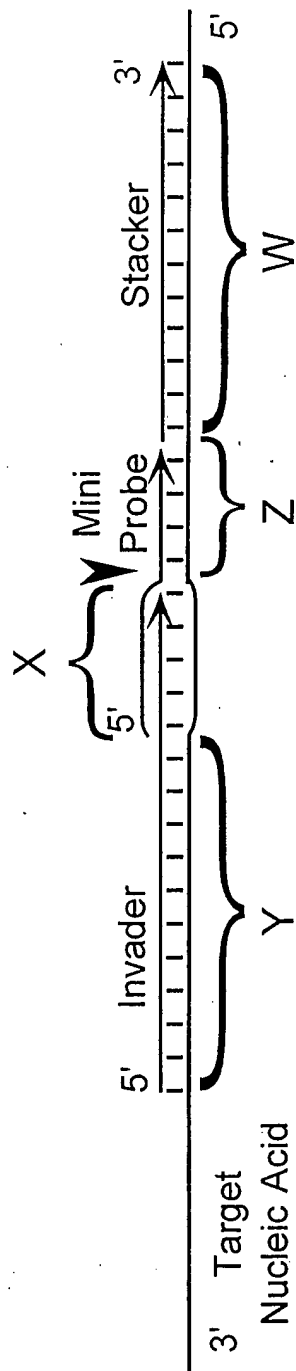
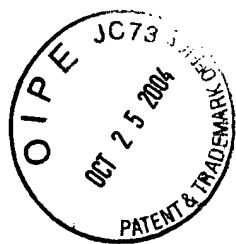


FIG. 57

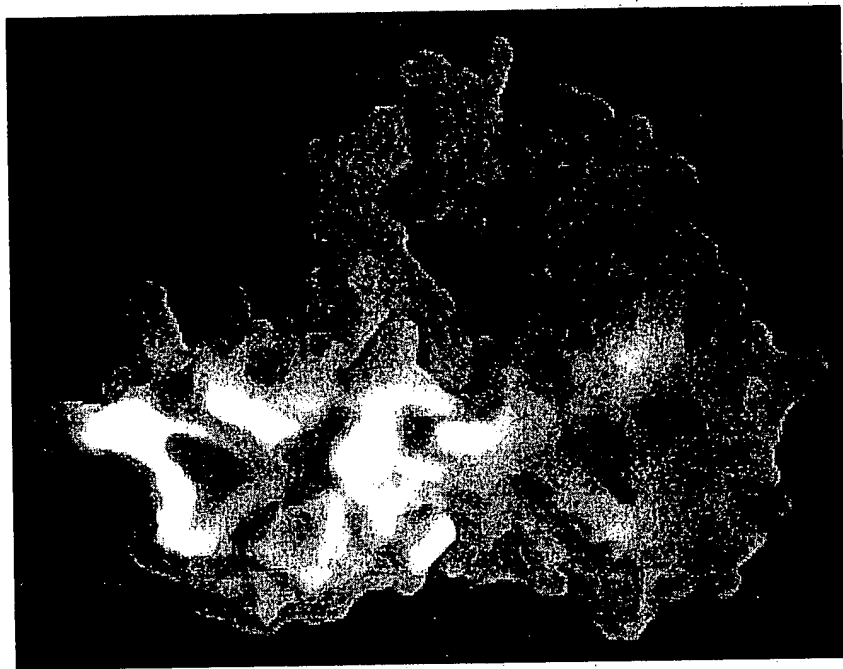
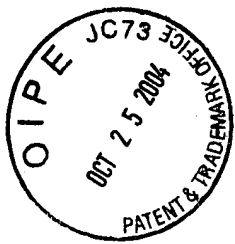
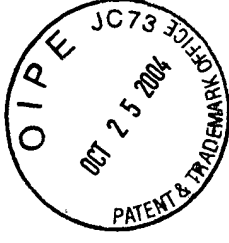


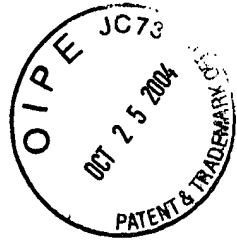
FIG. 58



	10	20	30	40	50	60	70									
1	MGVQ	-----	FGDFIPK	--	NIISFEDL	KGKKVAID	GMNALYQFLT	SIRLDGS	PLNRKGEIT	SAYNGVFY	MJAFEN1	.PRO				
1	MGVP	-----	IGEII	PR	--	KEIELENL	YGKKIAID	ALNAIYQFL	STIRQKDG	TPLMDSKGRIT	SHLSGLFY	PFUFEN1	.PRO			
1	MGIQ	LAKLI	ADVAPS	AIRENDI	KSYFGR	KVAID	ASMSIYQFL	IAVRQ	-GGDVL	QNEEGETT	SHLMGMFY	HUMFEN1	.PRO			
1	MGIH	LAKLI	ADVAPS	AIRENDI	KSYFGR	KVAID	ASMSIYQFL	IAVRQ	-GGDVL	QNEEGETT	S-LMGMFY	MUSFEN1	.PRO			
1	MGIK	GLNAI	IIEHVPS	AIRKSDI	KSF	FGRKVAID	ASMSLYQFL	IAVRQ	QDGGQL	TNEAGETT	SHLMGMFY	YST510	.PRO			
1	MGVH	SFWDI	AG	---	PTARP	VRLES	LEDKRM	AVDASI	WIYQFL	KAVRDQ	EGNAVK	---	SHITGFFR	YSTRAD2	.PRO	
1	MGVS	GLWN	I	---	PVKRP	VKLETL	VNKR	LADASI	WIYQFL	KAVRDQ	EGNQLKS	---	SHVVGFFR	SPORAD13	.PRO	
1	MGVQ	GLWK	L	---	CSGRO	VSPEAL	EGKIL	AVDISI	WLNQAL	KGVRDR	HGNSIEN	---	PHLLTLFH	HUMXPG	.PRO	
1	MGVQ	GLWK	L	---	CSGHR	VSPEAL	EGKVL	AVDISI	WLNQAL	KGVRD	SHGNVIEN	---	AHLLTLFH	MUSXPG	.PRO	
1	MGVQ	GLWK	L	---	CSGRP	INPGT	LEGKIL	AVDISI	WLNQAV	KGARDR	QGNAIQN	---	AHLLTLFH	XENXPG	.PRO	
1	MTINGI	WEWANH	V	---	RKVP	NETMRD	KTLSID	GHIWL	YESL	KGC	EAHHQQT	---	PNSYLVT	FTT	CELRAD2	.PRO

	80	90	100	110	120	130	140											
64	KTIH	LLENDIT	PIWV	FDGEP	PKLKEK	TRKVR	REMKEL	KMKEA	IKK	---	EDFEE	AAKYAKR	VSYLTP	MJAFEN1	.PRO			
64	RTIN	LMEAGI	KPVY	VDGEP	PEFKK	KELEK	RREARE	EEAEK	WREALEK	---	GEIEE	ARKYAQR	ATRVNE	PFUFEN1	.PRO			
70	RTIR	MMENGI	KPVY	VDGK	PPQL	KSGEL	AKRSERR	AEAEK	QLQQA	AA	---	GAE	OVEKFTKRL	VKVT	HUMFEN1	.PRO		
69	RTIR	MENGI	KPVY	VDGK	PPQL	KSGEL	AKRSERR	AEAEK	QLQQA	QEA	---	GME	EEVEKFTKRL	VKVT	MUSFEN1	.PRO		
71	RTL	MIDNGI	KPCY	VDGK	PPDL	KSHEL	TKRSS	RRVETE	KL	EA	---	TTE	LEKMKQERR	LKVS	YST510	.PRO		
61	RICK	LLYFGI	RPV	VDG	GVPL	KRET	IRQK	ERRQ	KRES	AKSTAR	KL	LALQL	QNGS	NDNKR	DSEVTM	YSTRAD2	.PRO	
61	RICK	LLFFGI	KPV	VDG	GAPSL	KRQTI	QKQARR	L	DREEN	ATVT	ANKLL	LALQ	MRHQ	AML	LKRDA	DEV	SPORAD13	.PRO
61	RLCK	LLFFRI	RP	IFV	DG	APLL	KKQTL	VKR	RQKDL	ASSDS	RKTTE	KL	KTFL	KRQAI	KTERIA	AATVTG	HUMXPG	.PRO
61	RLCK	LLFFRI	RP	IFV	DG	APLL	KKQTL	AKR	RQKDS	SASID	SRKTTE	KL	KTFL	KRQAL	KTDRIA	AASVTG	MUSXPG	.PRO
61	RLCK	LLFFRI	RP	IFV	DG	APLL	KKQTL	AKR	RQRTD	KASND	ARKTNE	KL	RTFL	KRQAI	KAERIA	AATVTG	XENXPG	.PRO
60	RIOR	LLEL	KI	PIV	VDN	INASS	SAHESK	DQNEF	VRKRR	SFGD	SPFTNLV	---	---	---	---	---	CELRAD2	.PRO

FIG. 59A



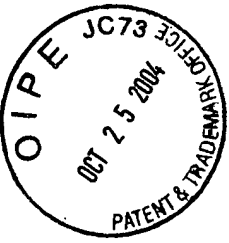
	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEM----						MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFGAPRLVRNLITITGKRKLPGK						PFUFEN1.PRO
136	QHNDCKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ						HUMFEN1.PRO
134	QHNDCKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ						MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTEAEQAQCAELAKKGVYAAASEDMDTLCYRTPFLLRHLTFSEAKKEPIH						YST510.PRO
131	DMIKEVQELLSRFGIPYITAPMEAEQAQCAELLQLNLVDGIITDDSDVFLFGGTKIYKNMFHEKNY----						YSTRAD2.PRO
131	VMIKECQELLRLFGLPYIVAPOEAEQAQCSKLLLEKLVDGIVTDDSDVFLFGGTRVYRNMFNQKNF----						SPORAD13.PRO
131	QMFLESQELLRLFGIPYIQAPMEAEQAQCAILDLTDTQTSGITDDSDIWLFGARHVYRNFFNKNKF----						HUMXPG.PRO
131	QMFLESQELLRLFGVPYIQAPMEAEQAQCAILDLTDTQTSGITDDSDIWLFGARHVYKNFFNKNKF----						MUSXPG.PRO
131	QMCLESQELLQLFGIPYIVAPMEAEQAQCAILDLTDTQTSGITDDSDIWLFGARHVYKNFFSQKNH----						XENXPG.PRO
111	DHVYKTNALLTELGIKVIIAPGDGEAQCARLEQLGVTSGCITTDIFYFLFGGKNLYRFDFTAGT-----						CELRAD2.PRO

	220	230	240	250	260	270	280
195	-----PELIELNEVLEDLRISLDDLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV						MJAFEN1.PRO
200	NVYVE-1KPELIILEEVLKELKTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF						PFUFEN1.PRO
206	EFHLSRILQELGLNQEQLVLCIILGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN-----KY						HUMFEN1.PRO
204	EFHLSRVLQELGLNQEQLVLCIILGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS-----KY						MUSFEN1.PRO
204	EIDTELVRGLDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKIKT--HGSIEKIVEFIESGESNNTKW						YST510.PRO
198	FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKMGMPVSSIEVIAEF--GNLKNFKDWYNNNGOFDKRK						YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFPDGTGLFEFKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNQLGLDRKNLINLAYLLGSDYTEGIPVGCVTAMEILNEFPGHGLEPLLKFSEWHEAQKNP						HUMXPG.PRO
119	YYQYVDFYSQLGLDRKNLINLAYLLGSDYTEGIPVGCVTAMEILNEFPGRGLDPLLKFSEWHEAQNNK						MUSXPG.PRO
198	YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPVGVVSAMEILNEFPGGQGLEPLVKFKEWSEAQKDK						XENXPG.PRO
175	-----SSTACLHDIHMLSLGRMF-----						CELRAD2.PRO

FIG. 59B

	290	300	310	320	330	340	350	
251	LKKEVEYYDEIKRIFKEPKV	-----	-----	-----	TD--	NYSLSLKLDPKEGIIKFLVDENDFN	YD	MJAFEN1.PRO
265	QKQSDVDLYAIKEFFLNPPV	-----	-----	-----	TD--	NYNLVWRDPDEEGILKFLCDEHDFSEE		PFUFEN1.PRO
269	PVPENWLHKEAHLFLEPEV	-----	-----	-----	LD	PESVELKWSEPNEEELIKFMCGEKQFSEE		HUMFEN1.PRO
267	PVPENWLHKEAQLFLEPEV	-----	-----	-----	VD	PESVELKWSEPNEEELVKFMCGEKQFSEE		MUSFEN1.PRO
272	KIPEDWPYKQARMLFLDPEV	-----	-----	-----	ID	GNEINLKWSPPEKELIEYLCDDKKFSEE		YST510.PRO
265	QETENKFEKDLRKKLVNNEI	ILDD	FPSVMVYDAYMRPEVD	HDTT	PFVW	GVDPDLMLRSFMKTQLGWPHE		YSTRAD2.PRO
268	KNDVNTPVKKRINKLVGK	-IIL	PSEFPNPLVDEAYLHP	AVDDSKQSFQW	GIPDLDEL	RQLMATVGSWKQ		SPORAD13.PRO
268	KIRPNPHTKVKKKL	--	RTLQLTPGFNP	PAVAEAYLKP	VDDSKGSFLW	GKPDLDKIREFCQRYFGWNR		HUMXPG.PRO
268	KVAENPYDTKVKKKL	--	RKLQLTPGFNP	PAVADAYLR	PVDDSRGSFLW	GKPDVDKIREFCORYFGWNR		MUSXPG.PRO
268	KMRPNPNDTKVKKKL	--	RLDLQ	QSFNP	AVASAYLKP	VDES	SAFSWGRPDLEQIREFCESRFGWYRL	XENXPG.PRO
194	-----	EKKVSRPHL	I	STAILLGCDYFOR	GVQNI	GIVSVFD-ILGEFGDDGNEEIDPHVILDRFASVYRE		CELRAD2.PRO
	360	370	380	390	400	410	420	
300	RVKKHVDKLYNLIA	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
314	RVKNGLERLKKAI	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
320	RIRSGVKRLSKSRQGS	-TQGR	LD	DDFFKVT	-----	-----	-----	HUMFEN1.PRO
318	RIRSGVKRLSKSRQGS	-TQGR	LD	DDFFKVT	-----	-----	-----	MUSFEN1.PRO
323	RVKSGISRLKKGLKSG	-IQGR	LD	GFFOVV	-----	-----	-----	YST510.PRO
335	KSDEILPLIRDVNKRKK	-----	-----	-----	-----	-----	KGKQ	YSTRAD2.PRO
337	RTNEVLLPVIQDMHKKOF	-----	-----	-----	-----	-----	VG	SPORAD13.PRO
336	KTDESILFPVLKQLDAQQT	QLRIDS	FFRLAQ	QEKEDAKRIKSQRL	NRAVTCMLRKEKEAA	SEIEAVSVAM		HUMXPG.PRO
336	KTDESILYPVLKHLNAHQ	TLRIDS	FFRLAQ	QEKQDAKL	IKSHRLSR	AVTCMLRKEE	EKAPELTKVTEAM	MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQT	QLRIDS	FFRLAQ	HEAAG--	--LKSQRL	RRRAVTCMKR	KERDVEAE	EVEAAVAM
257	EIPARSED	TQRLRLRRKKYN	FPVGF	PNCD	AVHNAITMYLR	PPVSSEIPKI	IPR-----	AANFQQVAEIM
								CELRAD2.PRO

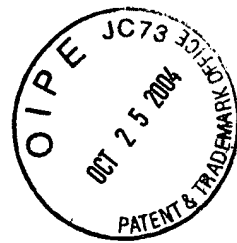
FIG. 59C



	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----	YST510.PRO
357	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
406	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
406	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
403	-----	-----	-----	-----	-----	-----	XENXPG.PRO
322	-----	-----	-----	-----	-----	-----	CELRAD2.PRO

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	-----	NKTKQKTL
327	-----	-----	-----	-----	-----	-----	KSGKQSTL
352	-----	-----	-----	-----	-----	-----	KKKAKTGAAG
350	-----	-----	-----	-----	-----	-----	KKKAKTGGAG
354	-----	-----	-----	-----	-----	-----	NKKLNKNKNK
364	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
429	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
476	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
469	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
458	-----	-----	-----	-----	-----	-----	XENXPG.PRO
387	-----	-----	-----	-----	-----	-----	CELRAD2.PRO

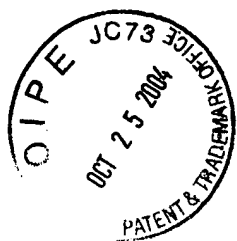
FIG. 59D



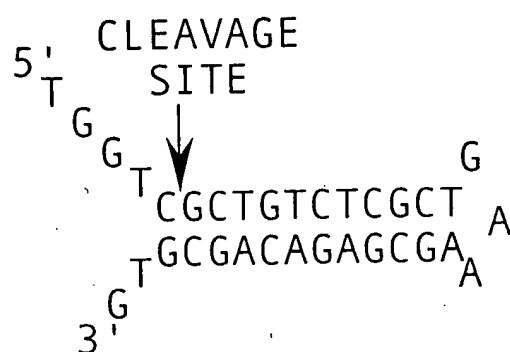
322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 ---RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

FIG. 59E



S-33



11-8-0

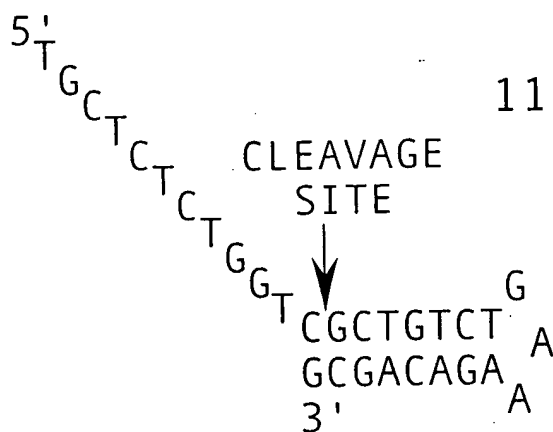


FIG. 60

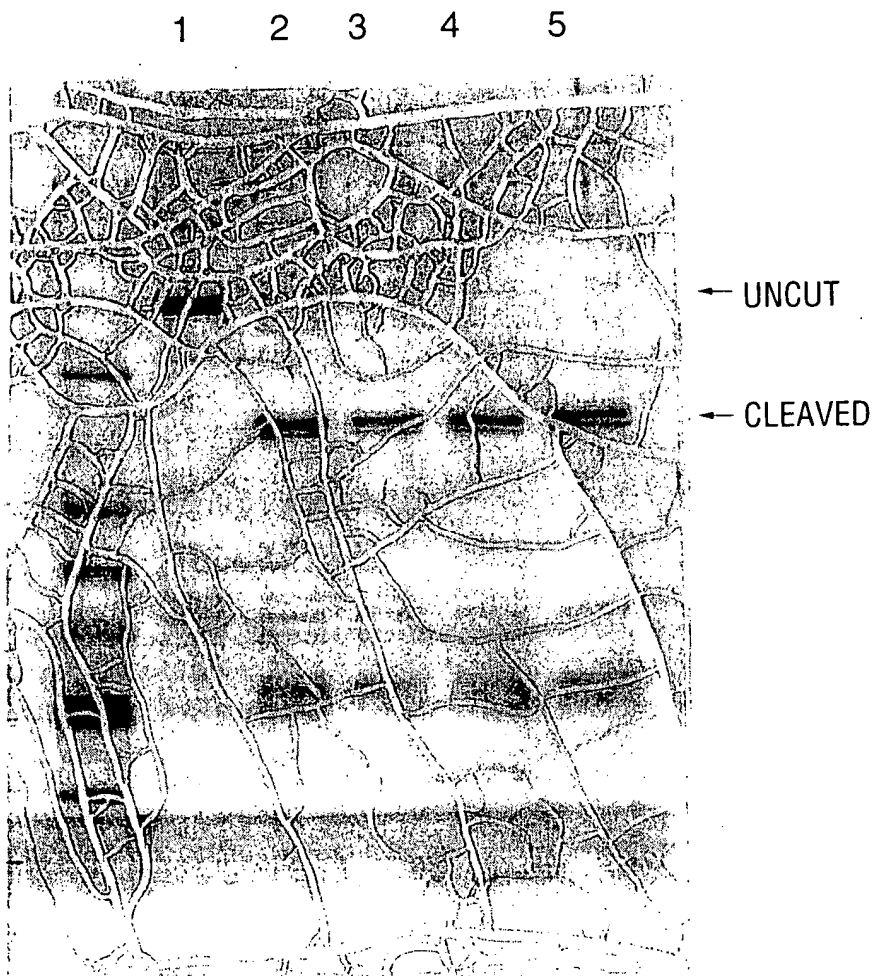
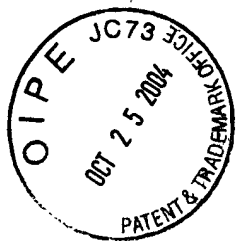


FIG. 61

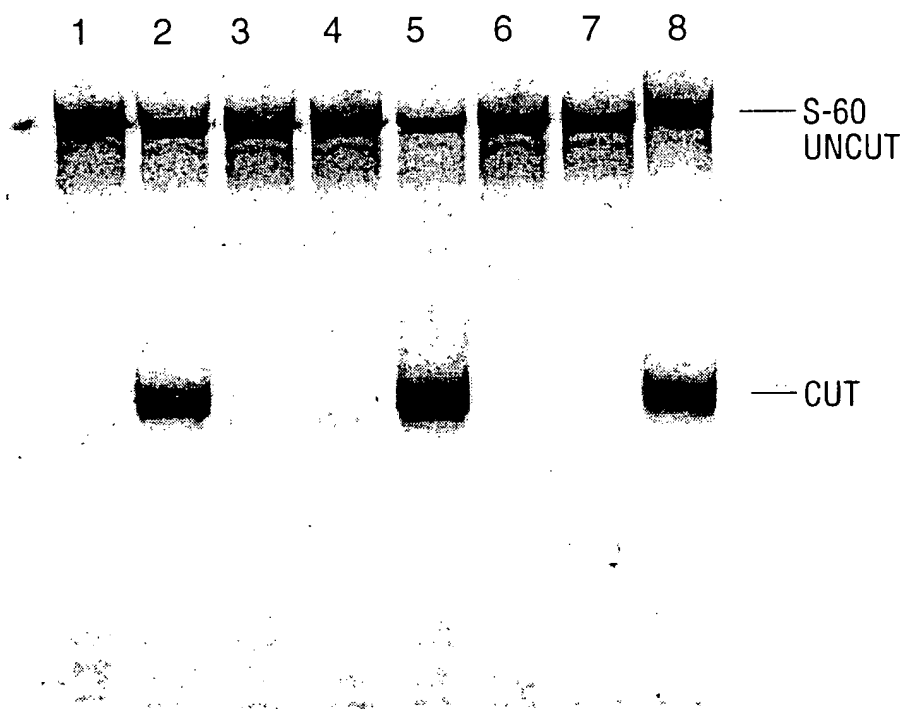
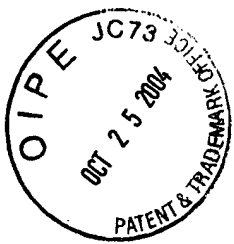


FIG. 62

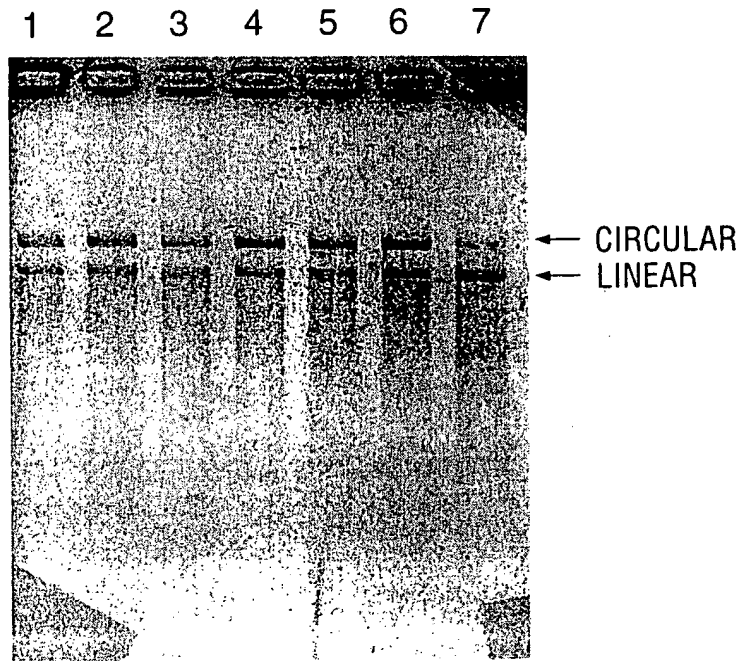
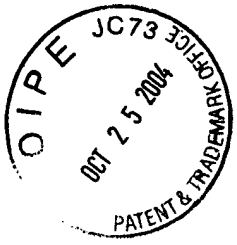


FIG. 63

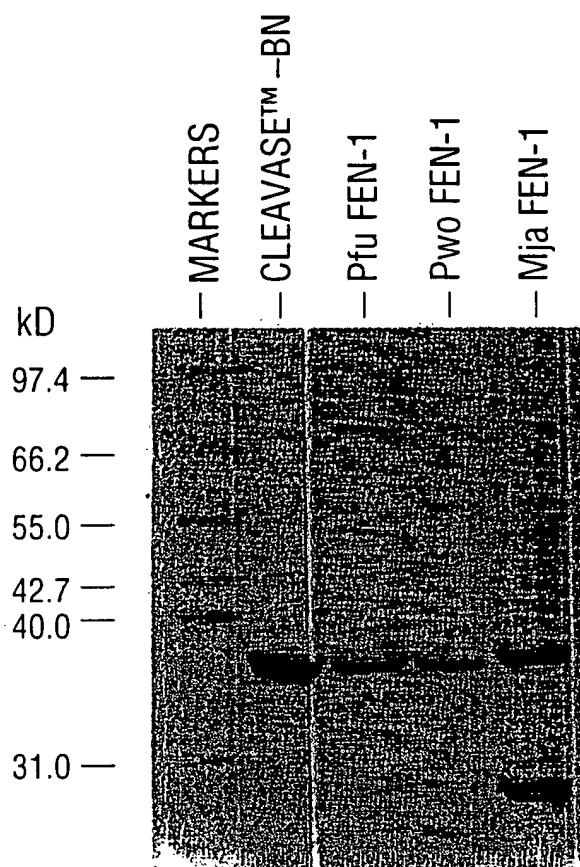


FIG. 64

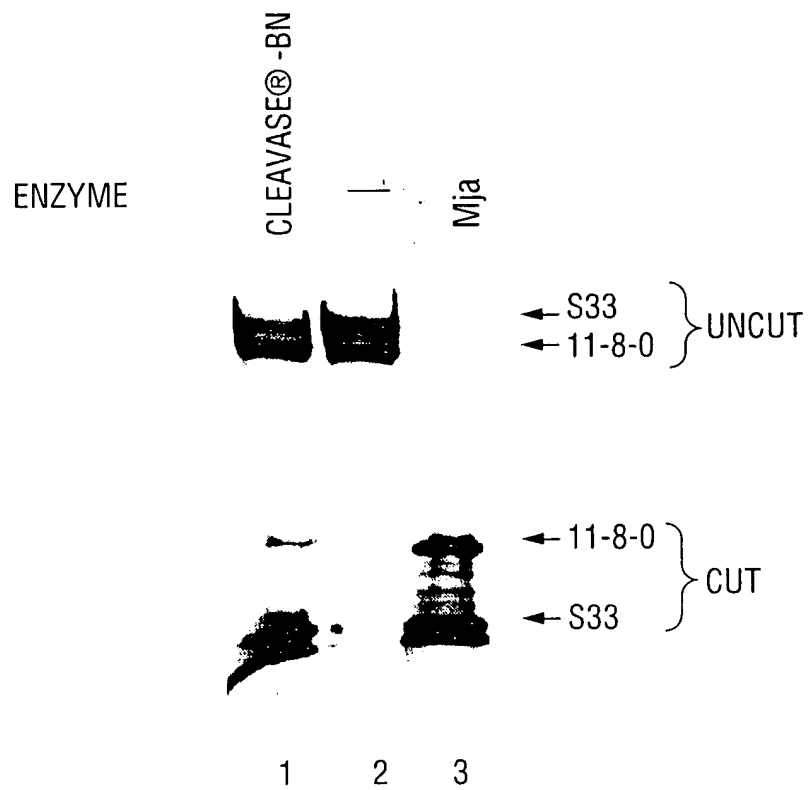
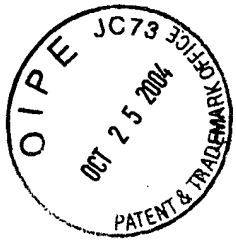
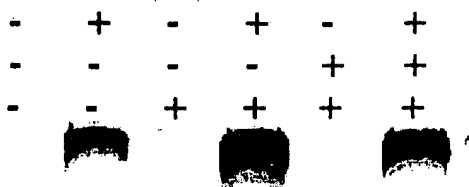
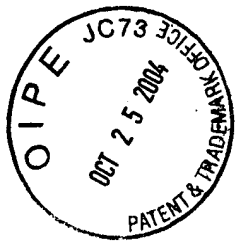
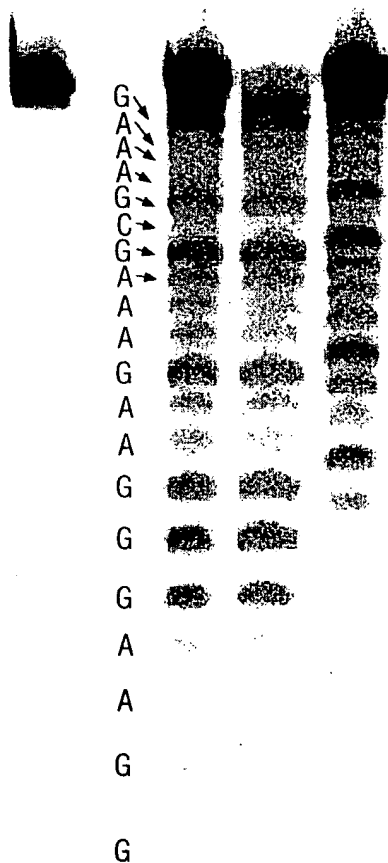


FIG. 65



TERMINAL TRANSFERASE
 ALKALINE PHOSPHATASE
 THERMAL DEGRADATION



5'-nAGAAAggaagggaagaaagcgaaagG-3'

FIG. 66

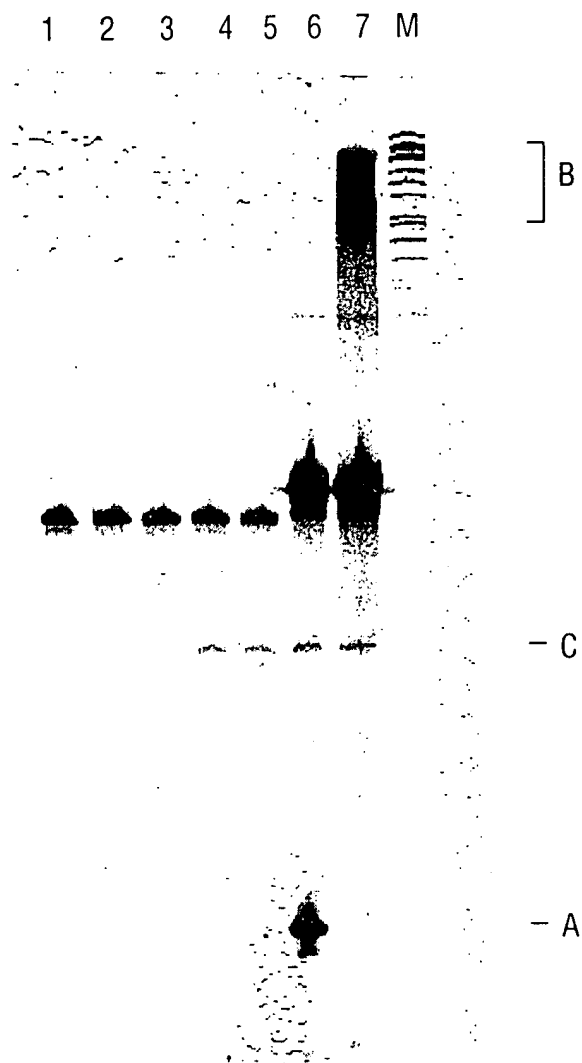
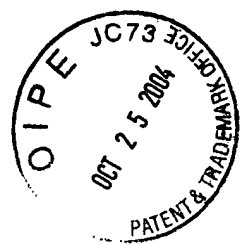


FIG. 67

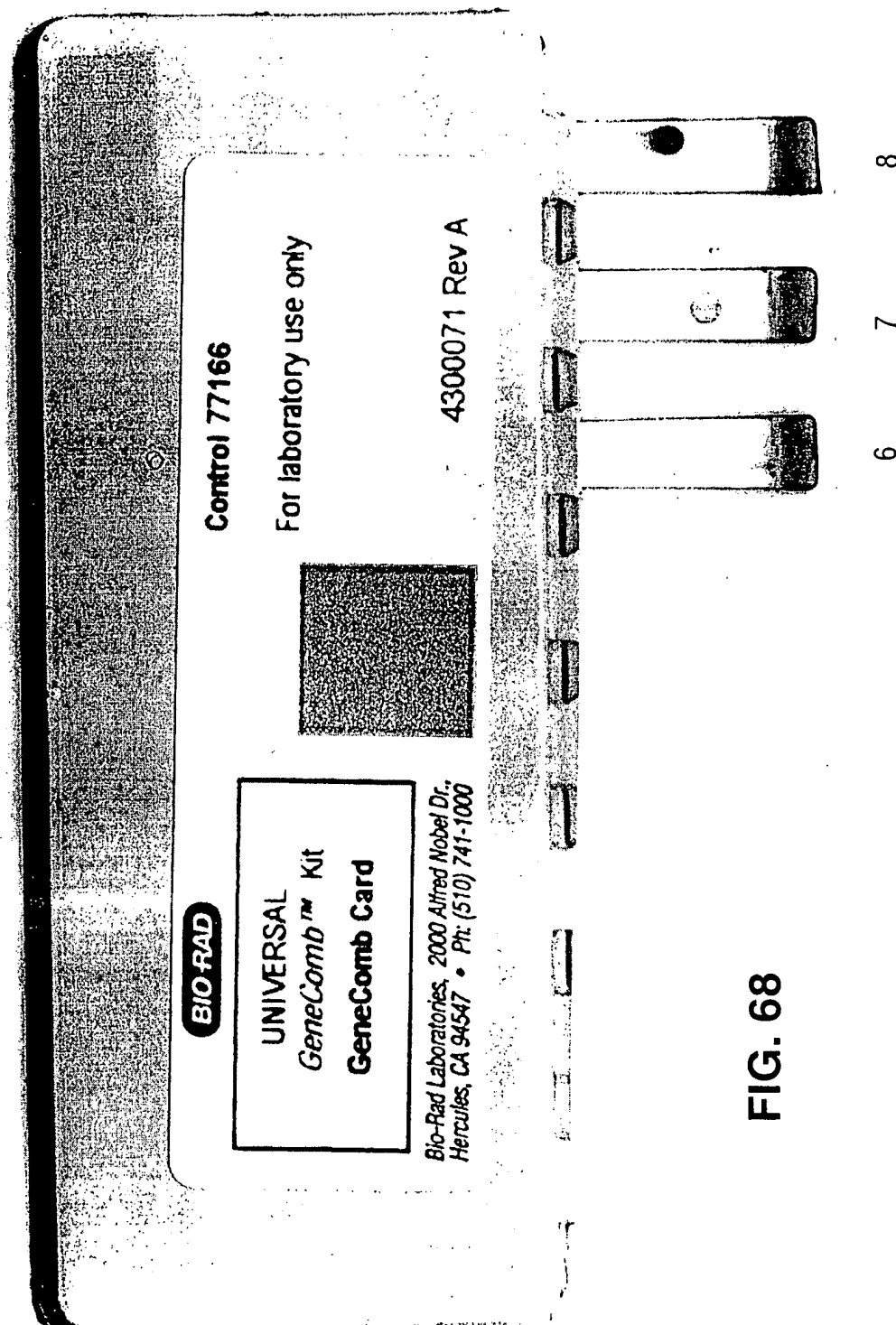
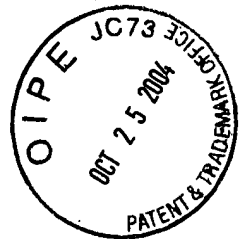


FIG. 68

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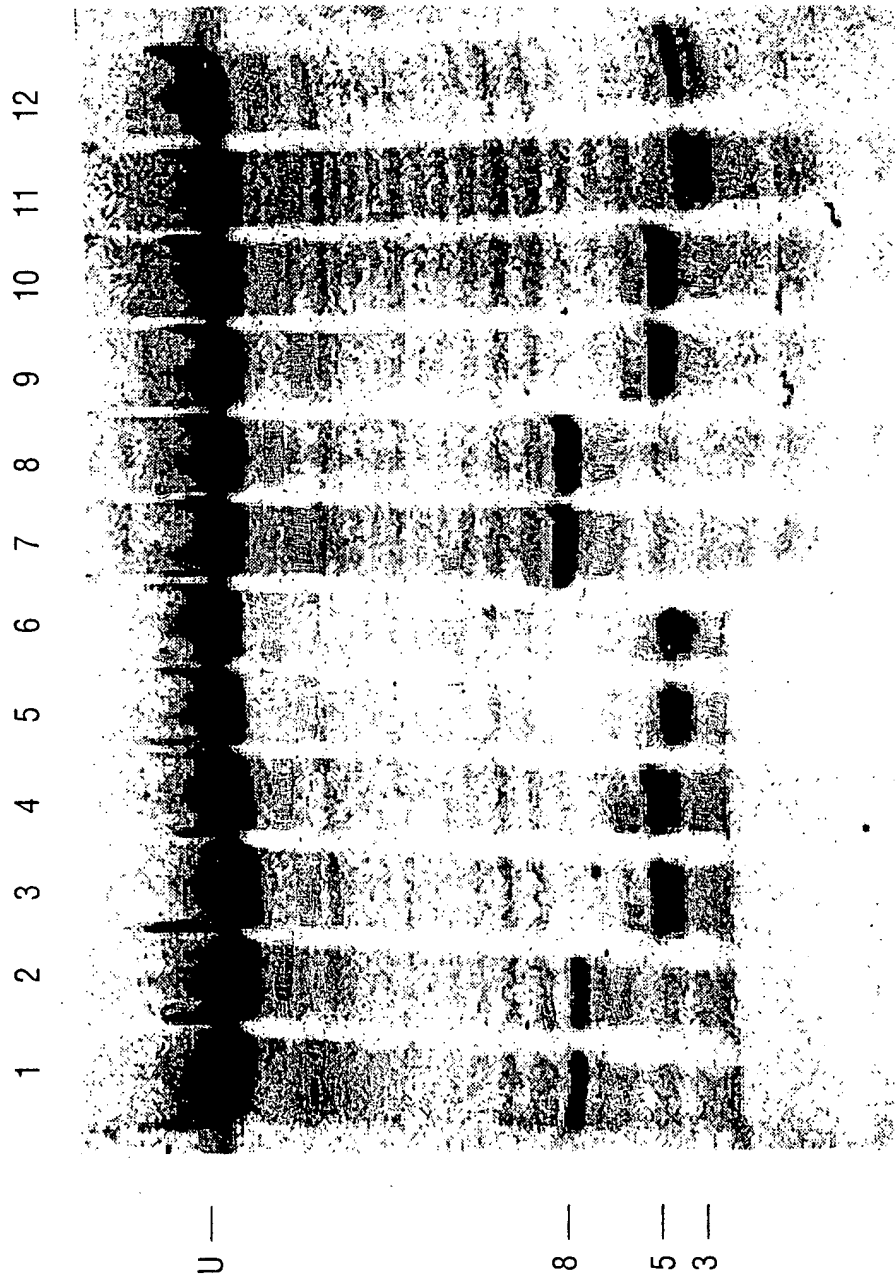


FIG. 69

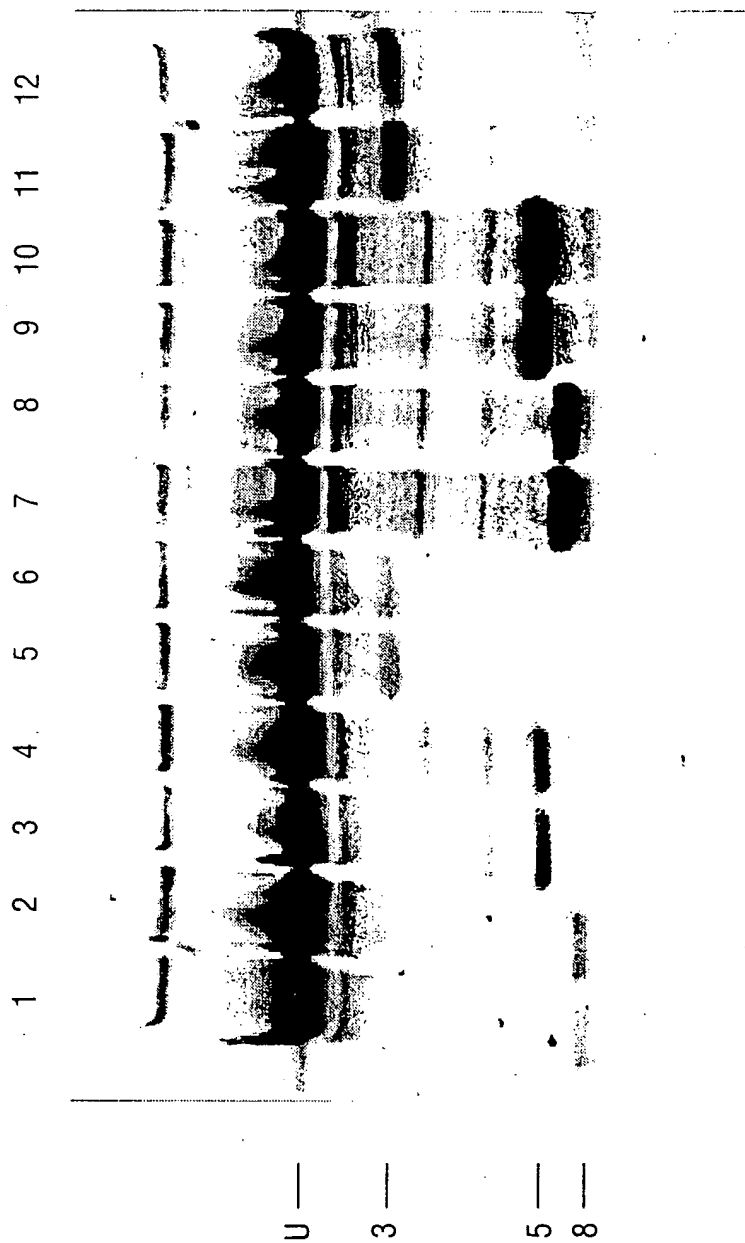
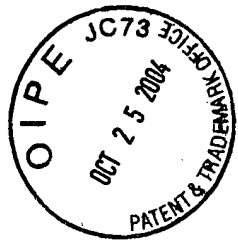


FIG. 70

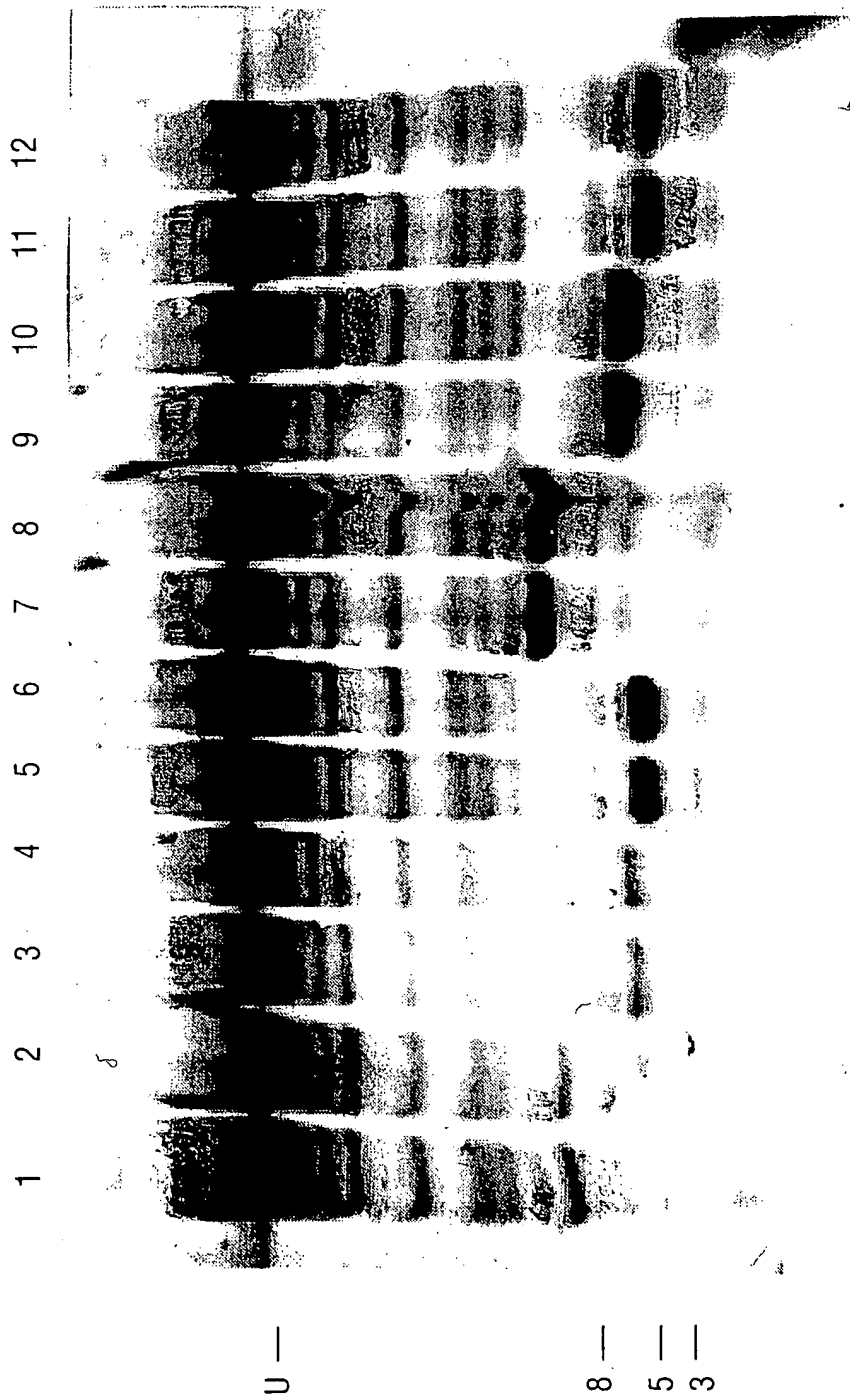
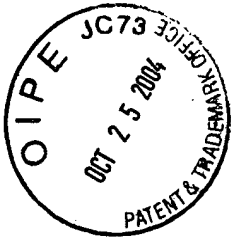


FIG. 71

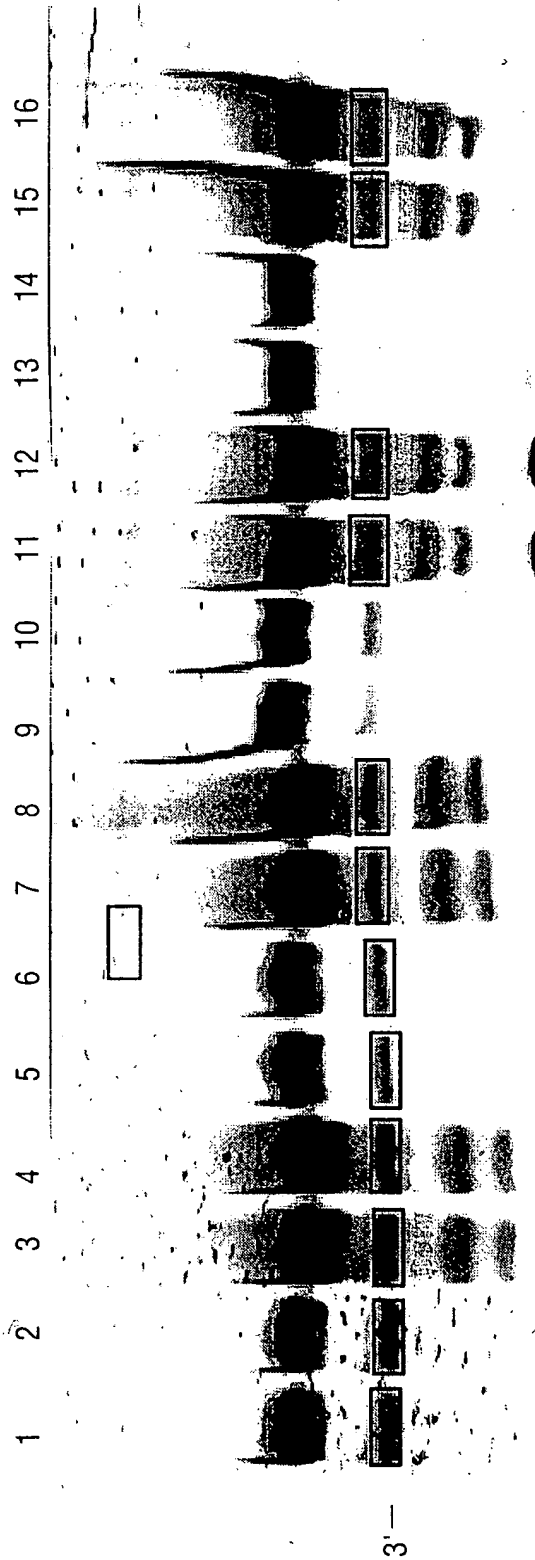


FIG. 72A

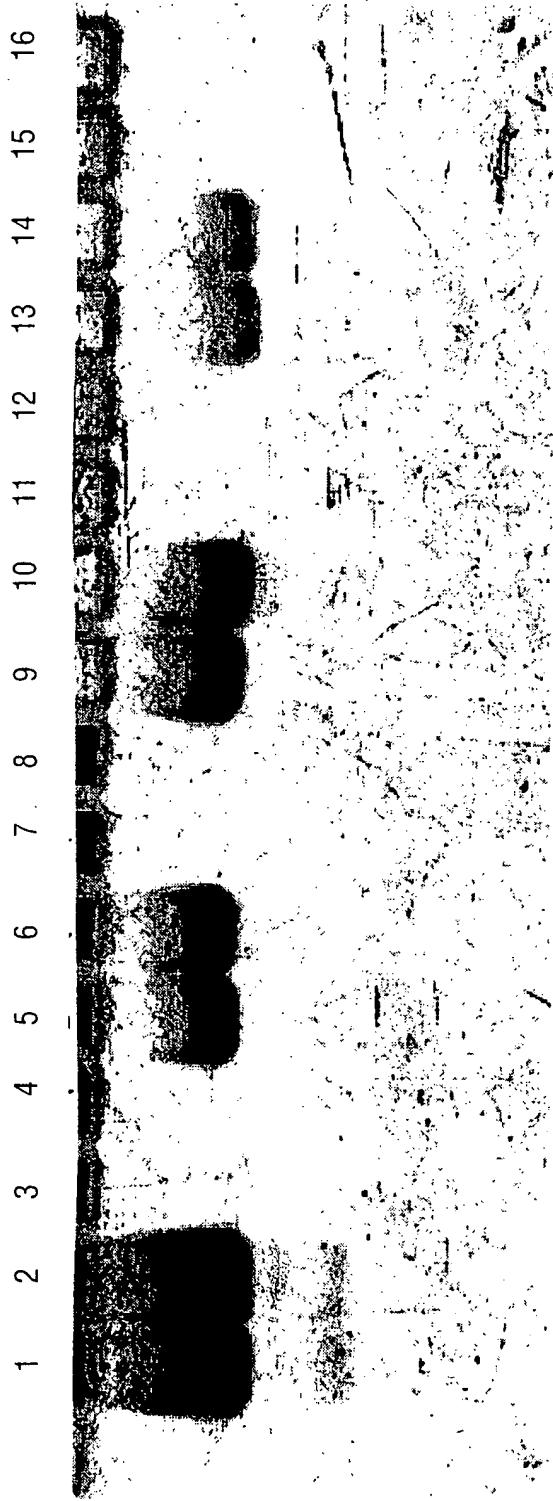
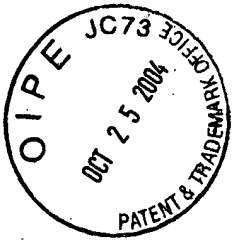


FIG. 72B

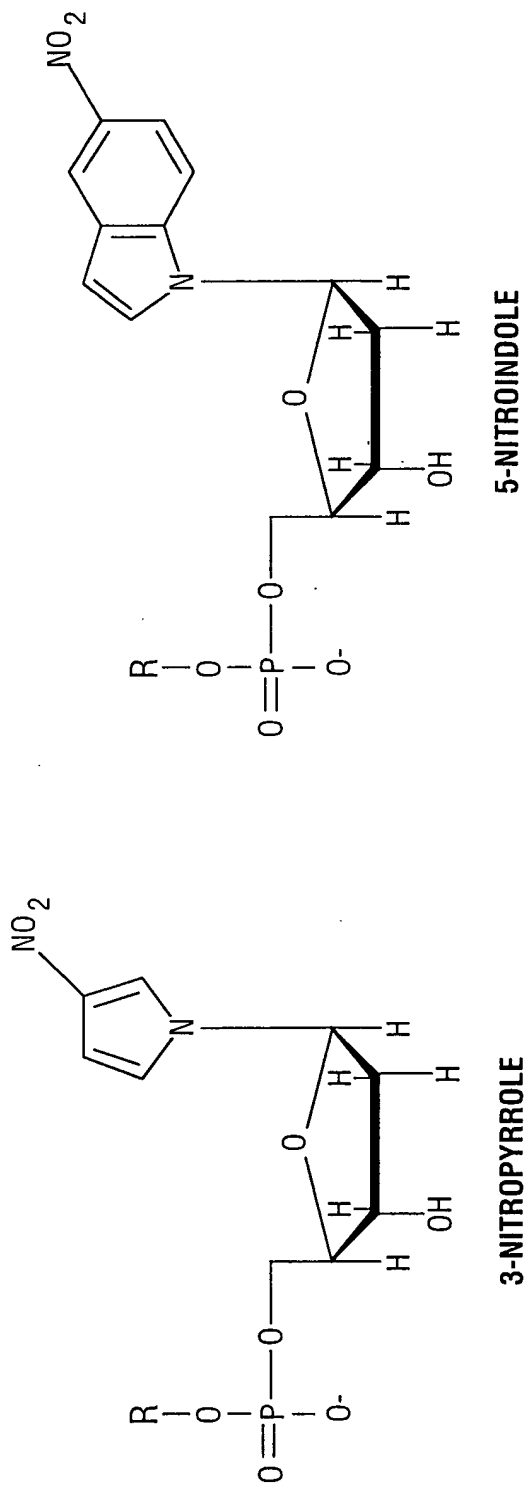
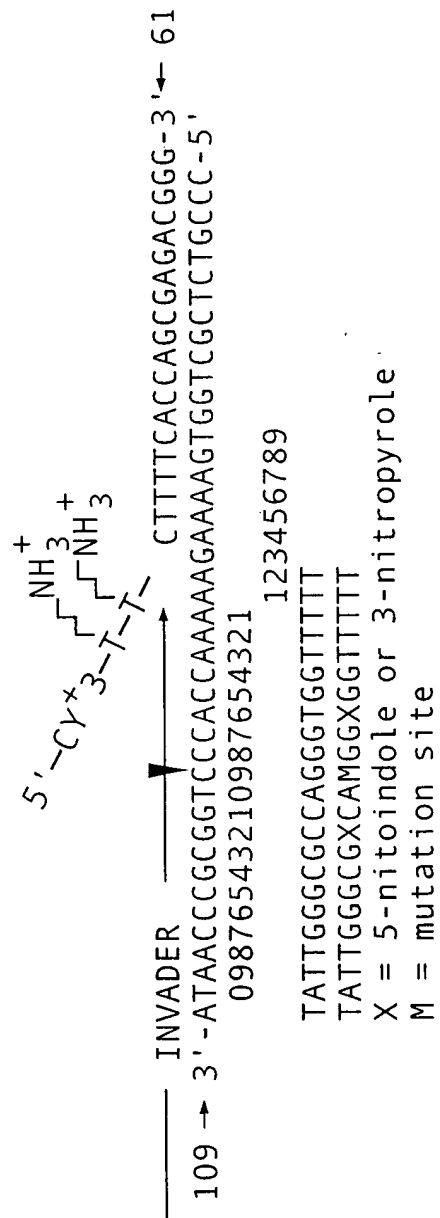


FIG. 73



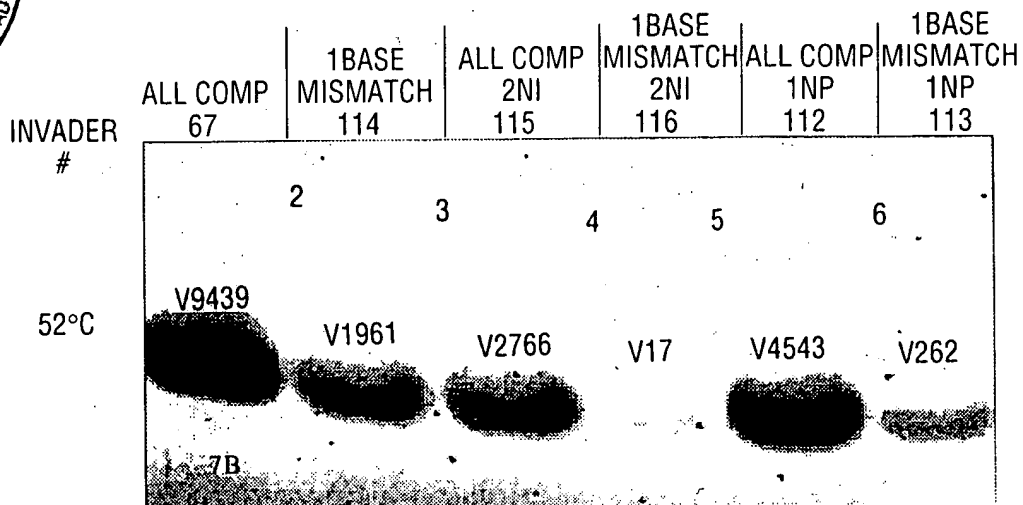
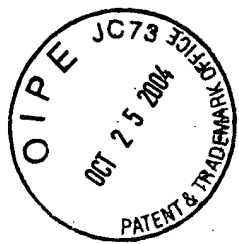


FIG. 75A

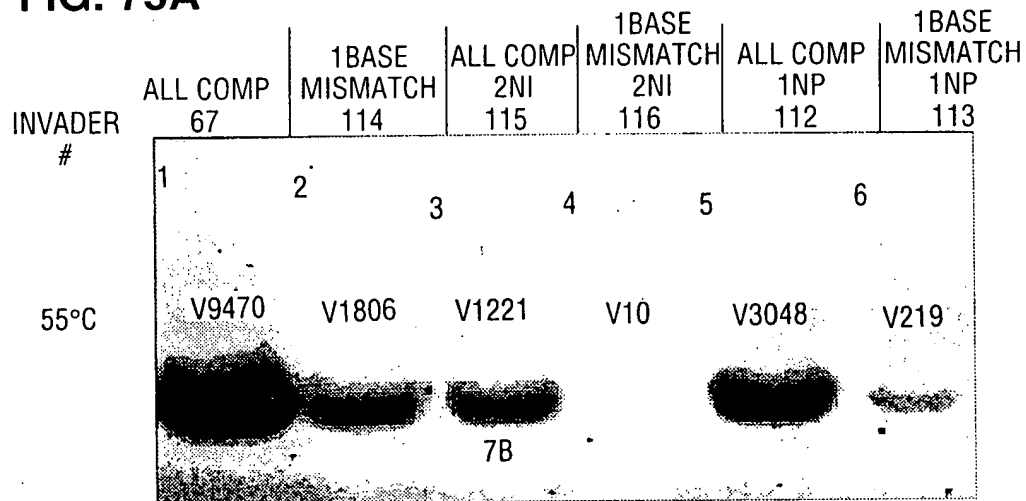
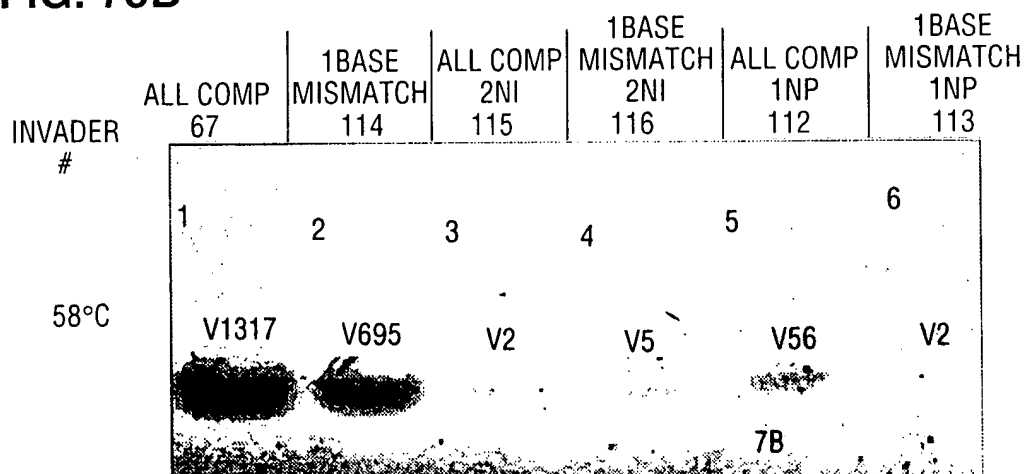


FIG. 75B



$$\begin{array}{c}
 \text{5' - } \text{CY}_3^+ \text{ - } \text{T}^+ \text{ - } \text{T}^+ \text{ - } \text{CACCAG} \text{ - } 161 \\
 \downarrow \\
 \text{3' - GCAGTTCGTGAGAACGGATGCXGTGGTCGAGGTTGATGGTTCAAATATAAGTC - 5'} \\
 \text{162 } \blacktriangleright \text{GCTCAAGGCACCTCTTGCCCTACGA} \quad \text{CITCCAACACTACCACAAGTTTATATTCAG} \blacktriangleleft \text{164}
 \end{array}$$

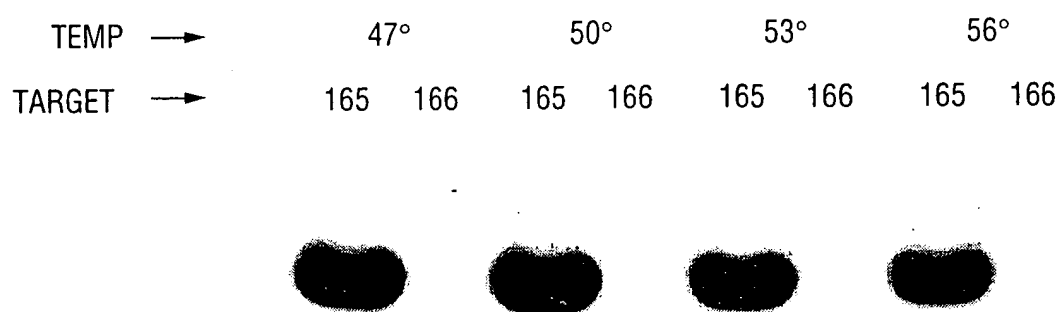
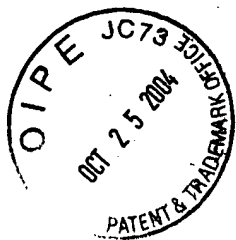
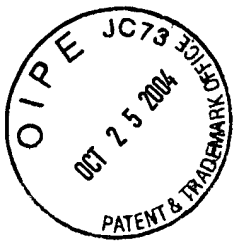


FIG. 77



F1
5' GTTCTCTGCTCTCTGGT 1819
CGCTGTCTCGCTTGT^G_A
GCGACAGAGCGAACA^A
3' GCTCTCTGGT

FIG. 78A

F1
5' GTTCTCTGCTCTCTGGT 2122
CGCT GTCTCGCTTGT^G_A
3' GCTCTCTGGTGCGACAGAGCGAACA^A
5' CGAGAGACCGCT^G
P15

FIG. 78B

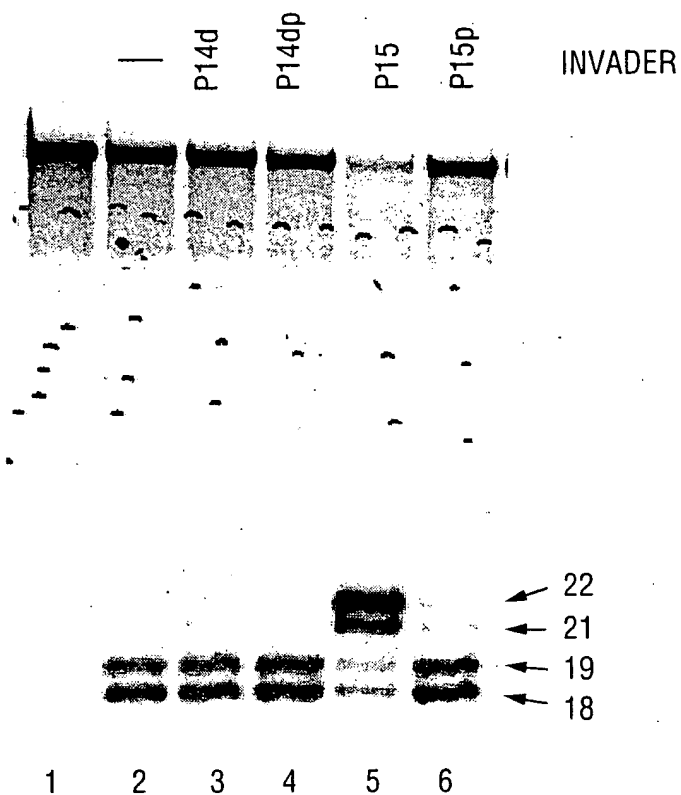


FIG. 78C

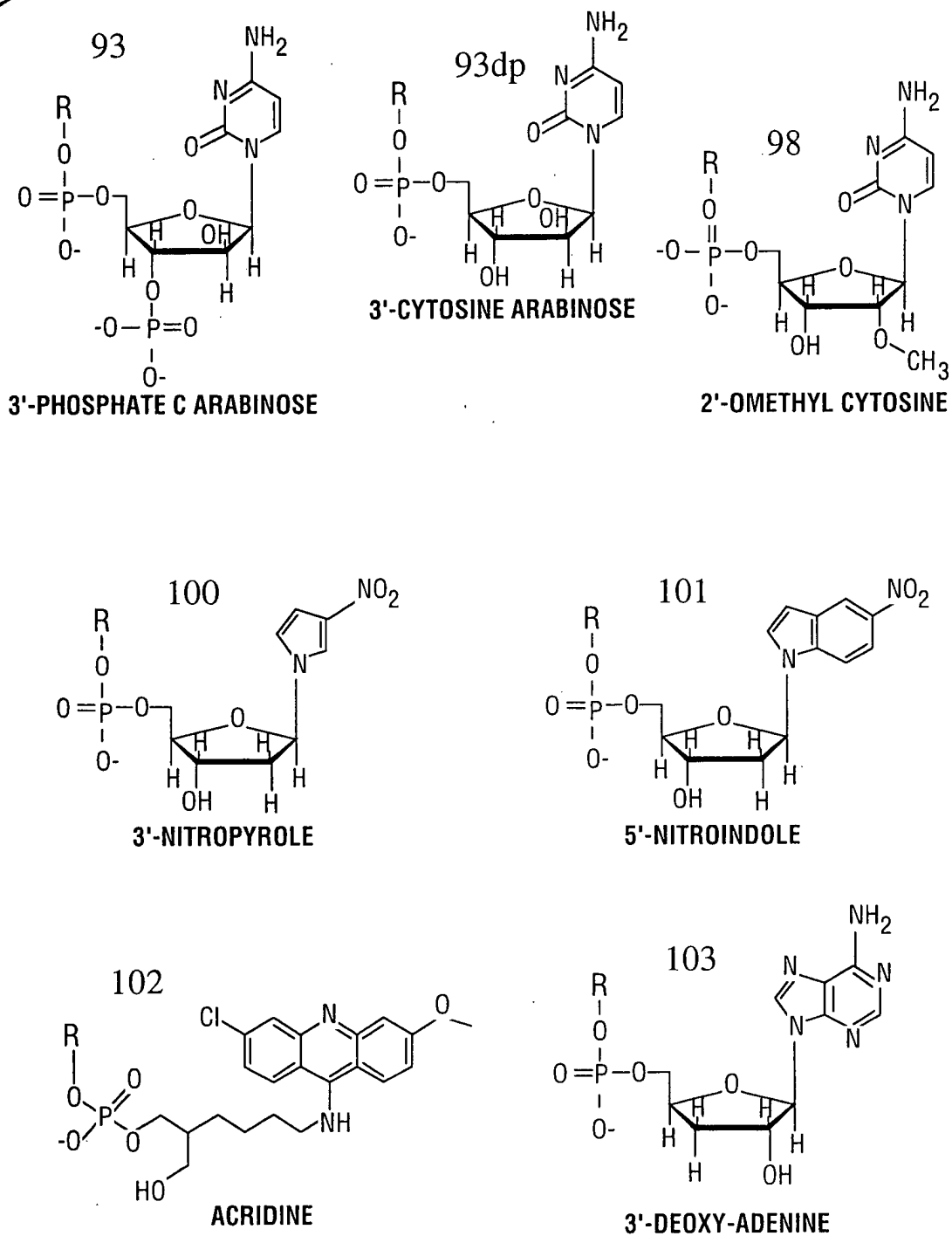
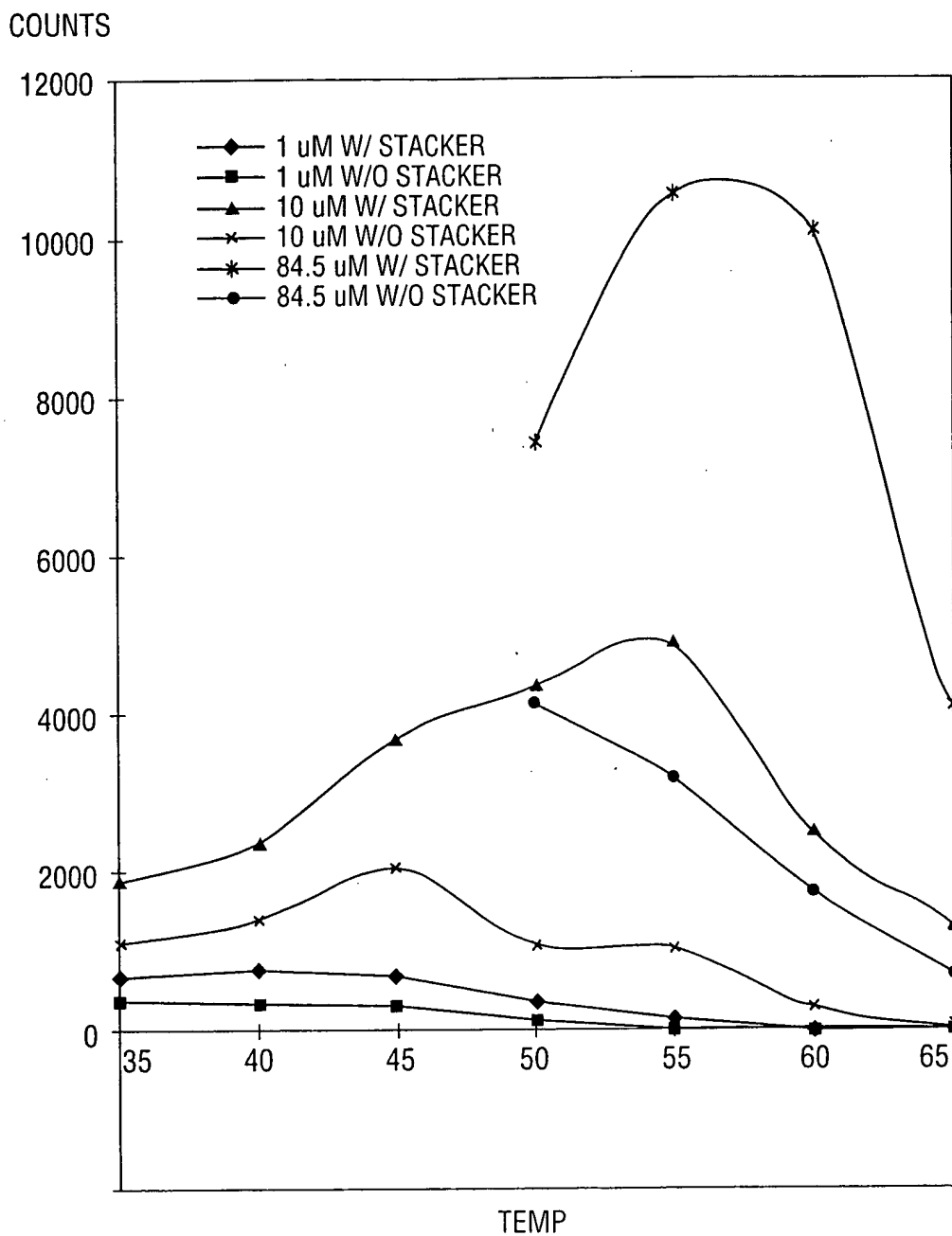
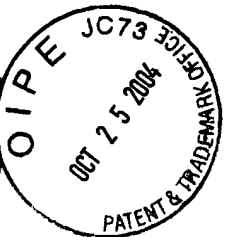


FIG. 79



CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIG. 80

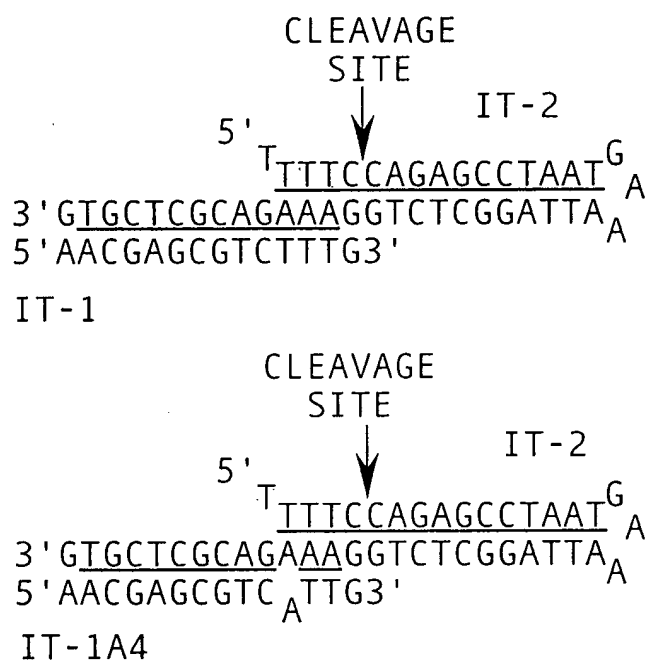
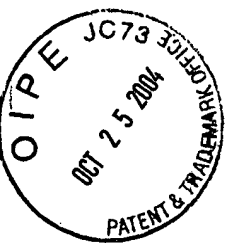


FIG. 81

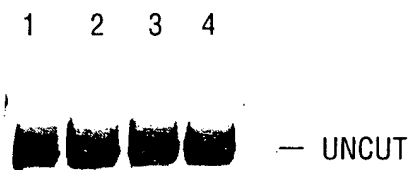
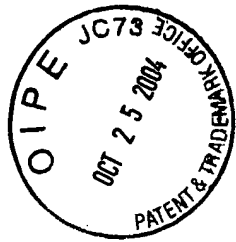


FIG. 82

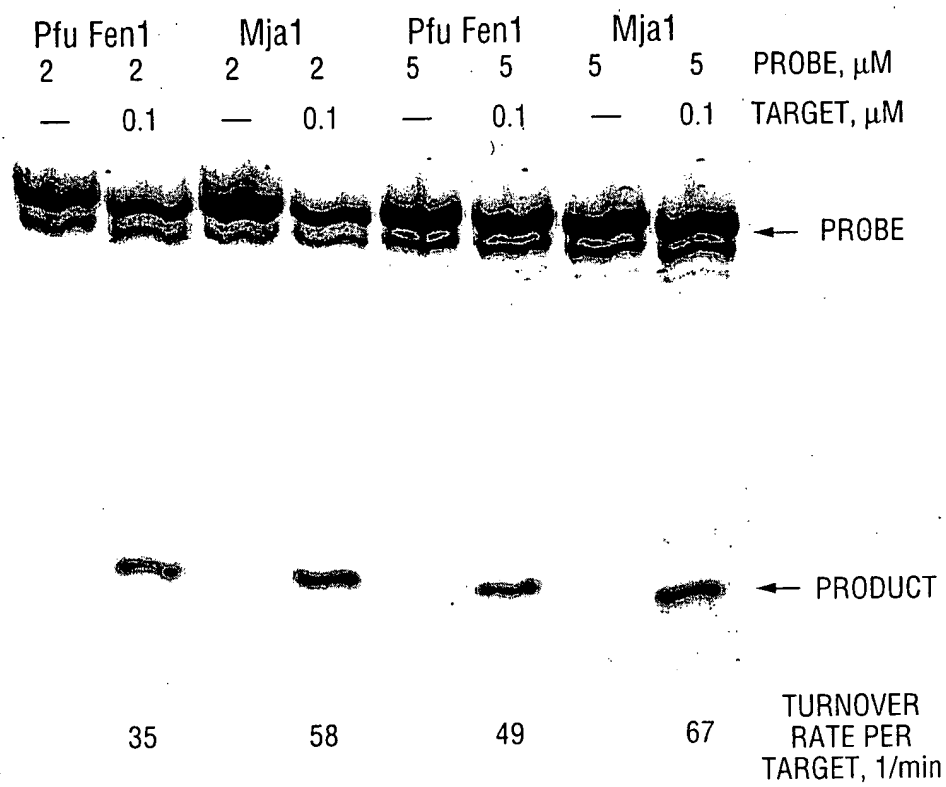
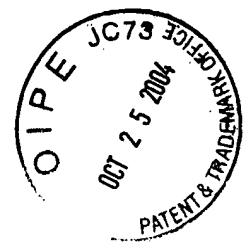
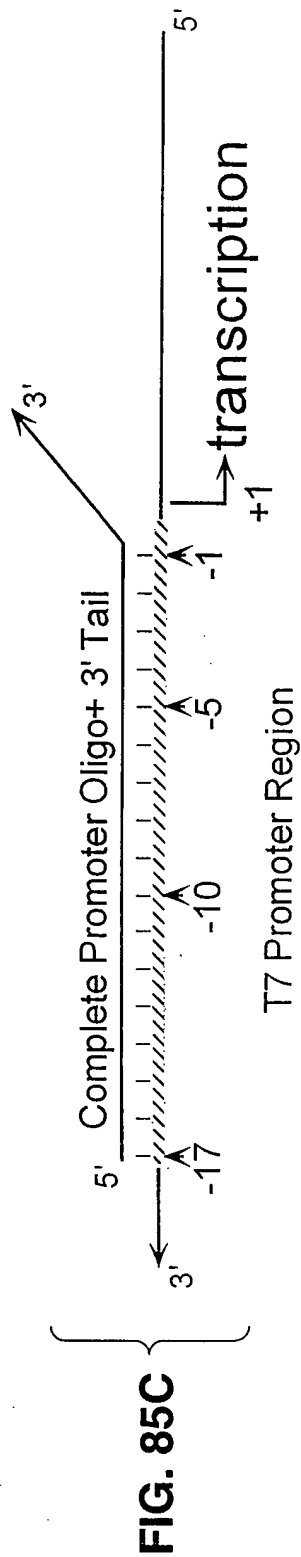
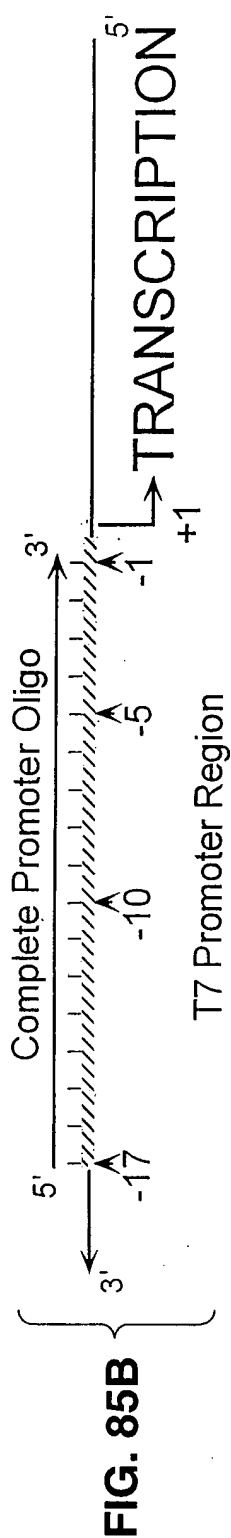
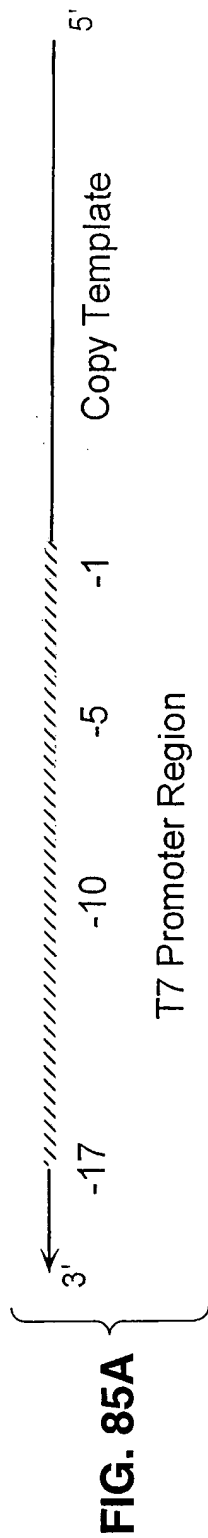


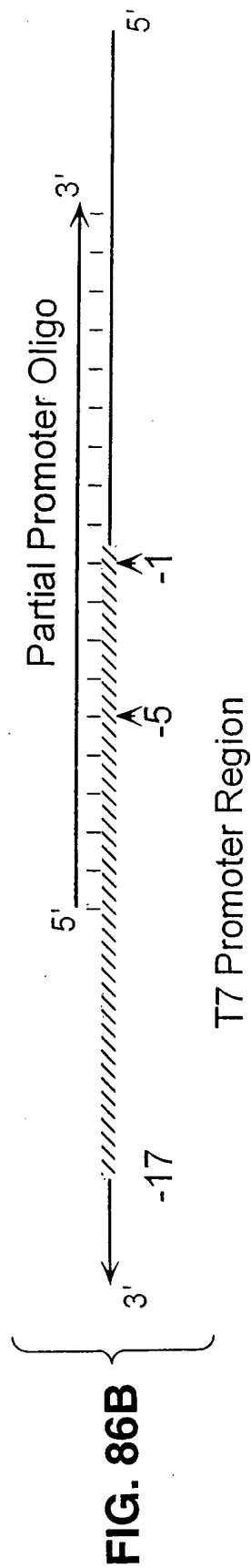
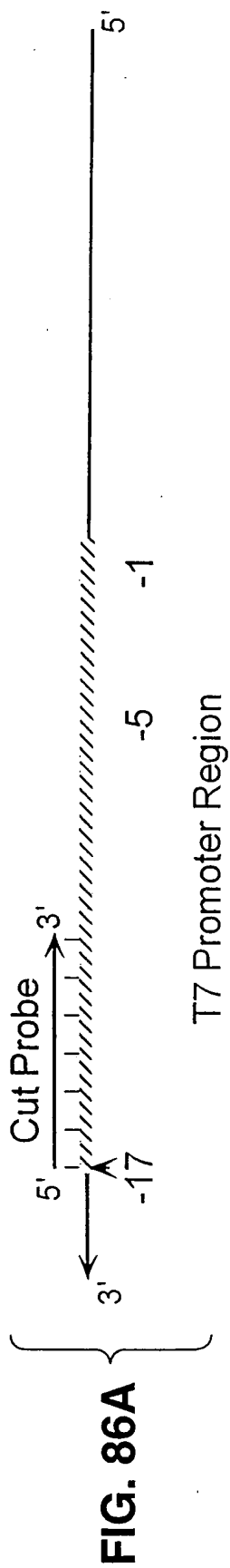
FIG. 83

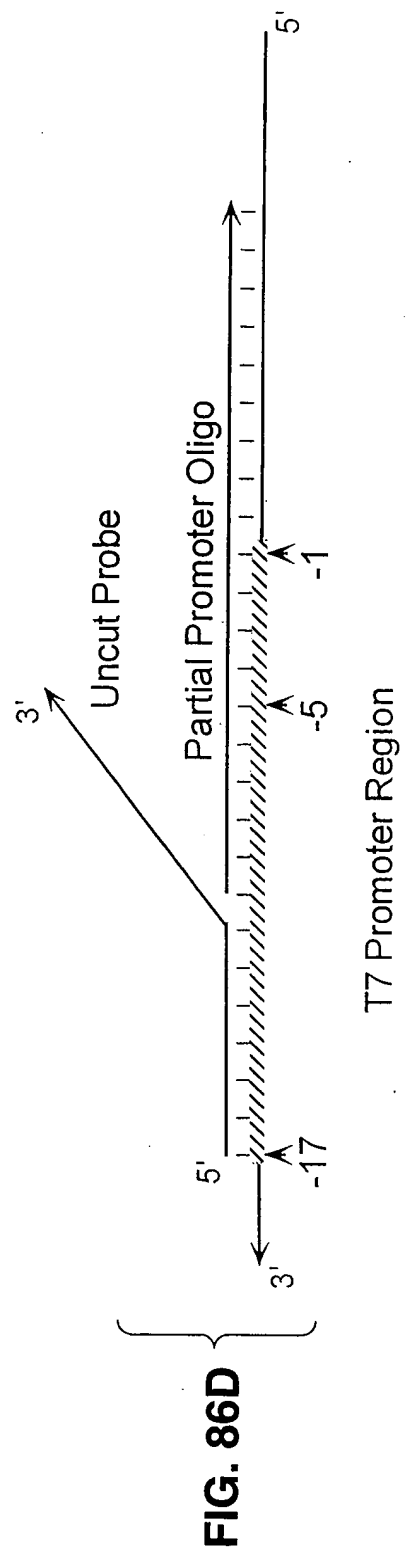
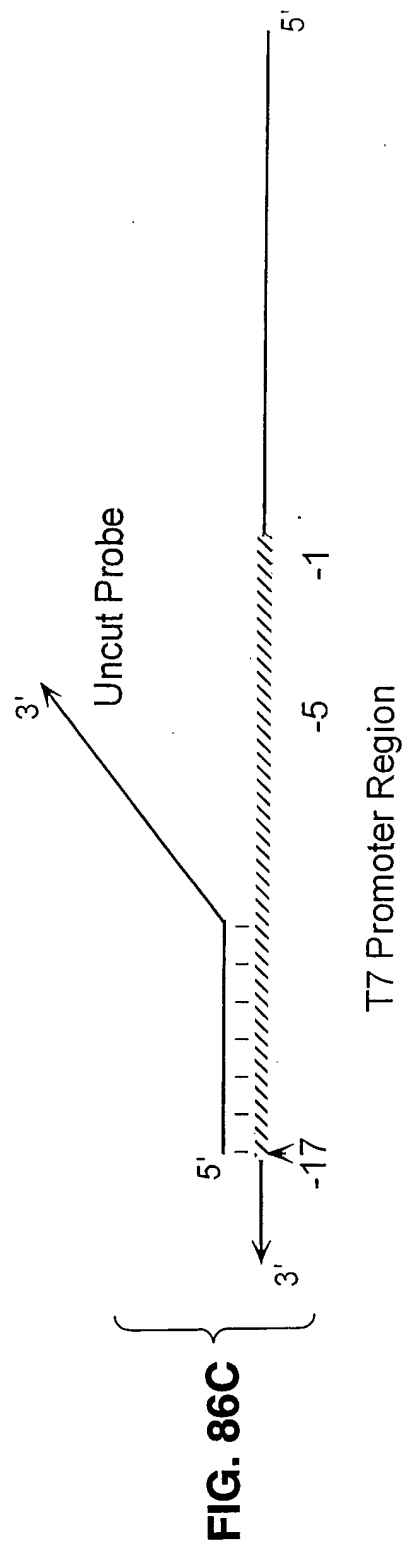
1 2 3 4 5



FIG. 84







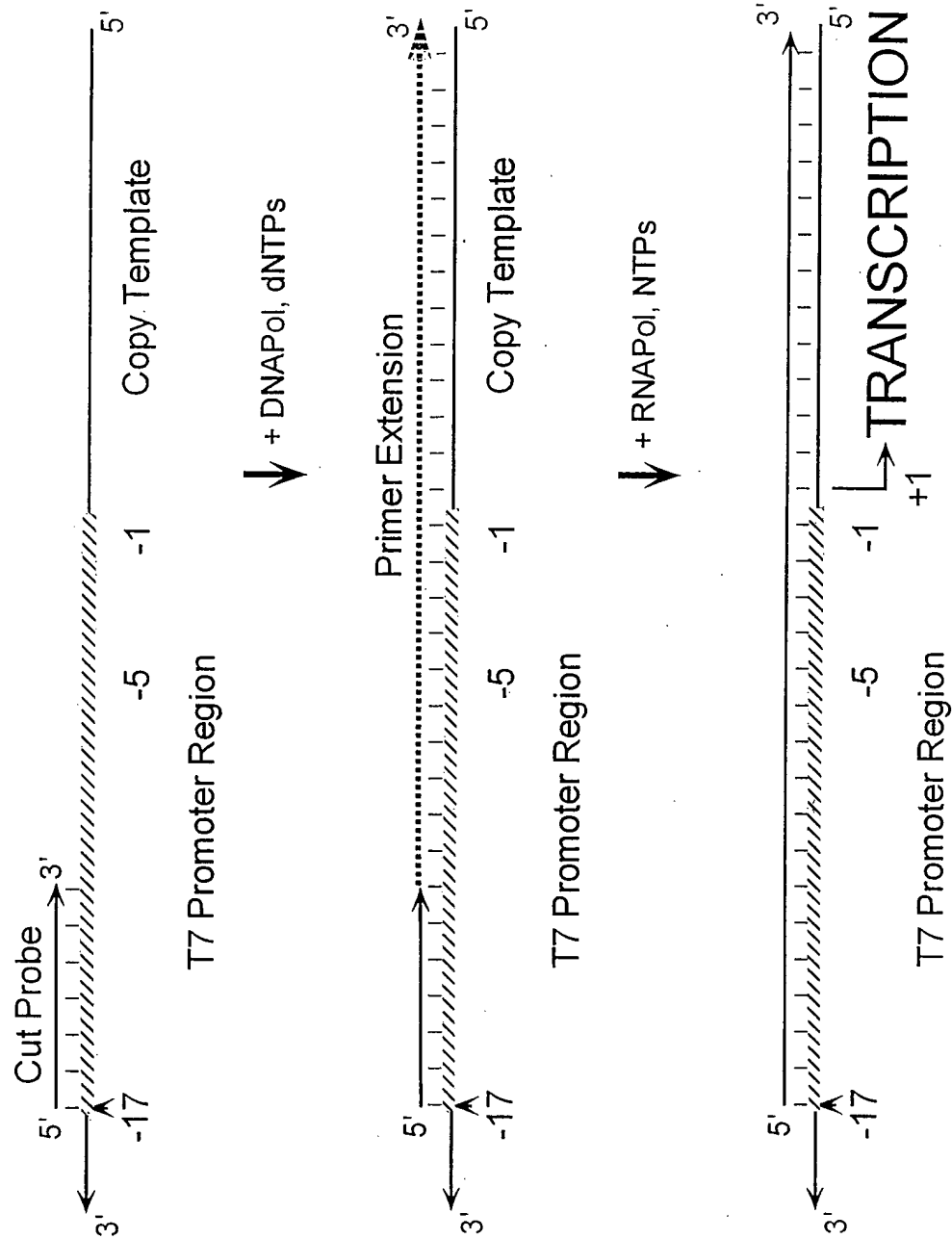


FIG. 87

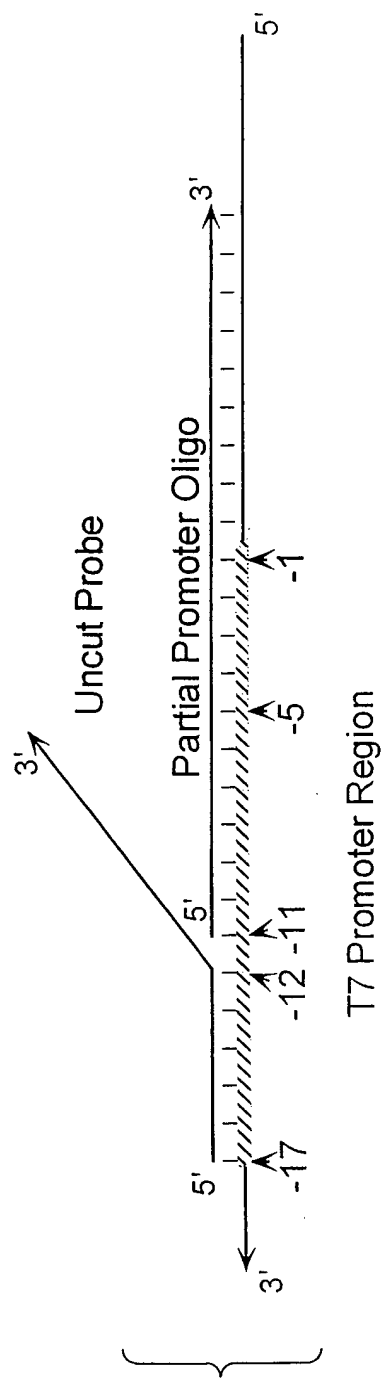


FIG. 88A

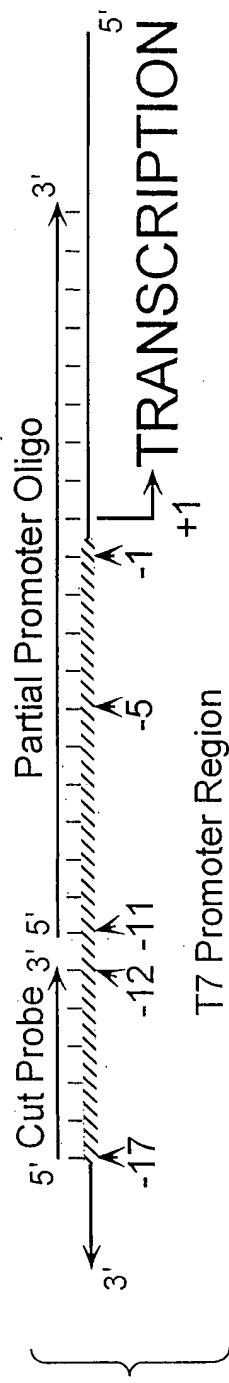


FIG. 88B

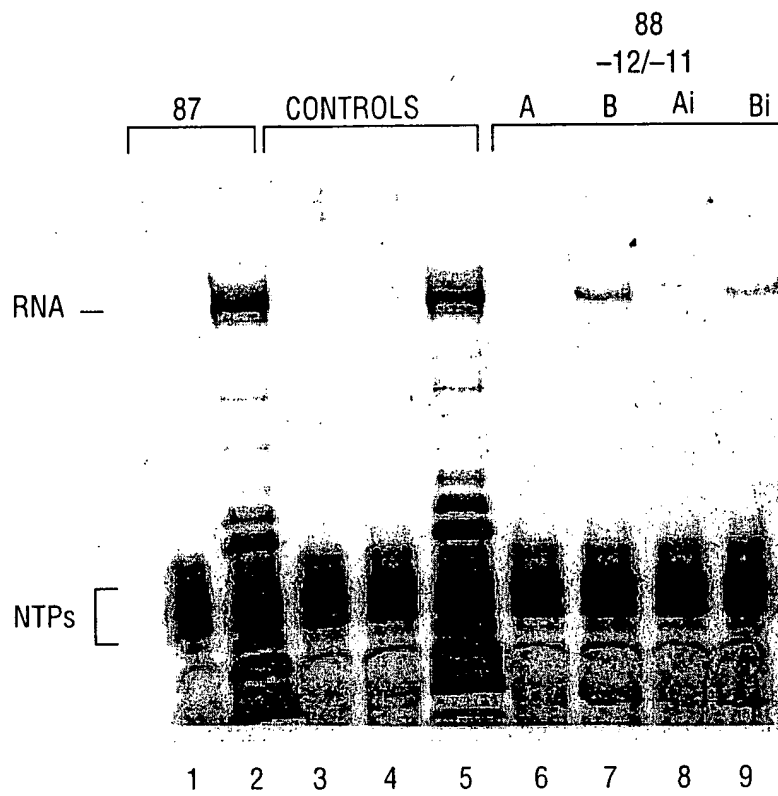
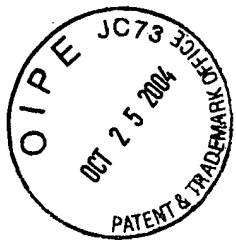


FIG. 89

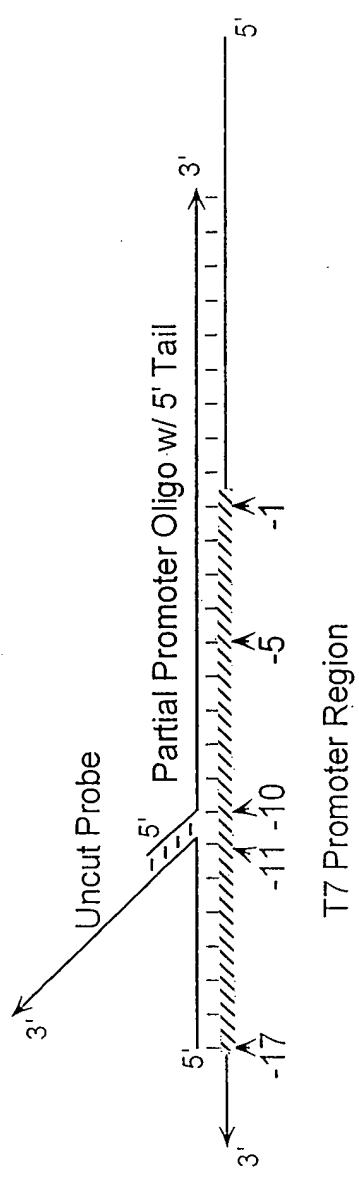


FIG. 90A

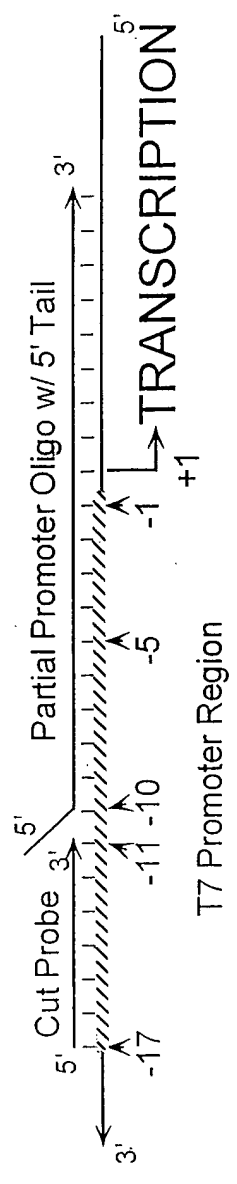


FIG. 90B

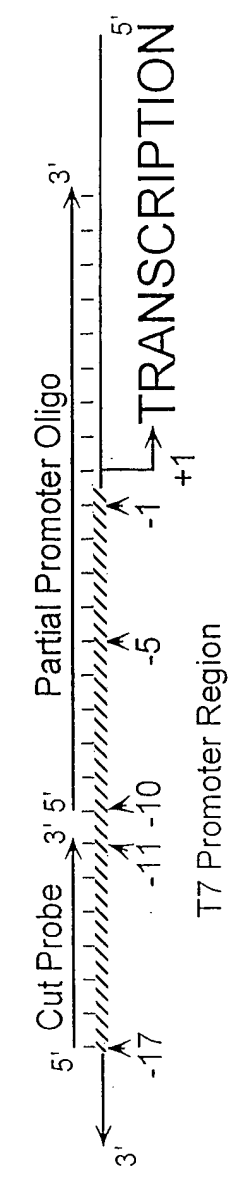


FIG. 90C

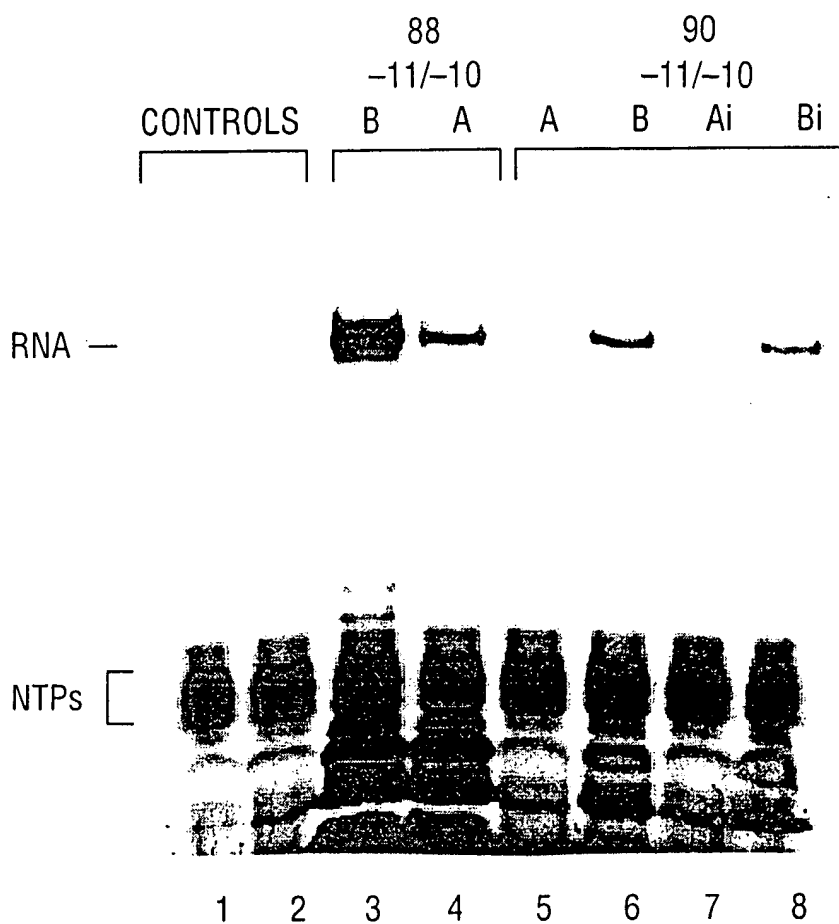
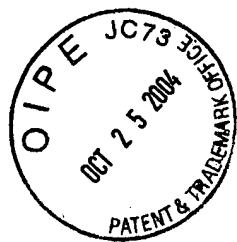


FIG. 91

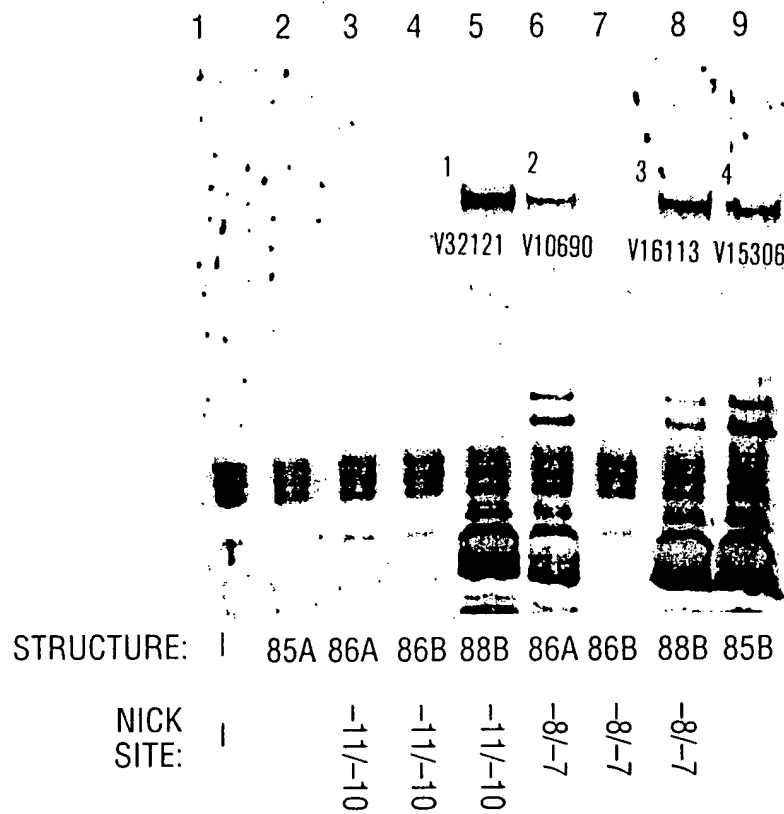


FIG. 92

{
 {
 {

FIG. 93A

1
 3'-gctttaattatgctgagtgatatccagaagataacctccagttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

↔

FIG. 93B

2
 5'-cgaataataacgactcactata-3'
 3'-gctttaattatgctgagtgatatccagaagataacctccagttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

↗

FIG. 93C

3
 #073-065
 5'-cgaataataacgactcactataccagaa-3'
 3'-gctttaattatgctgagtgatatccagaagataacctccagttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

4 NO DNA

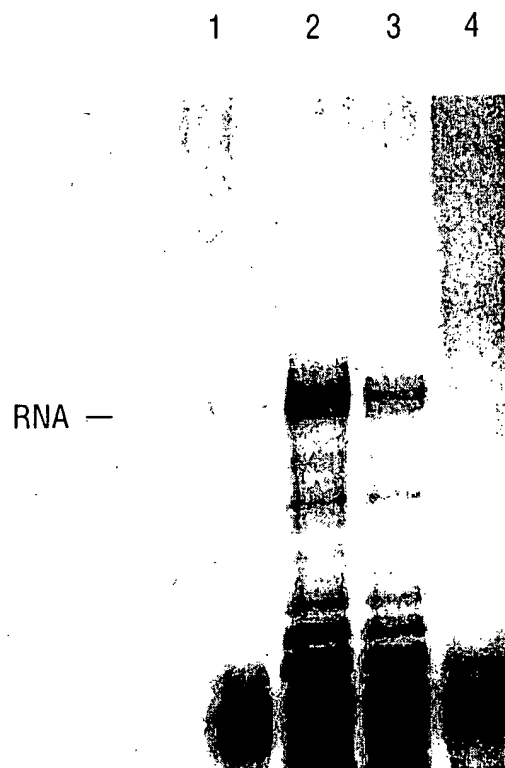
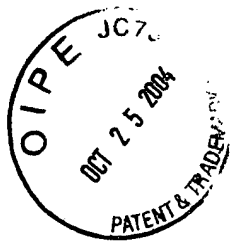


FIG. 93D

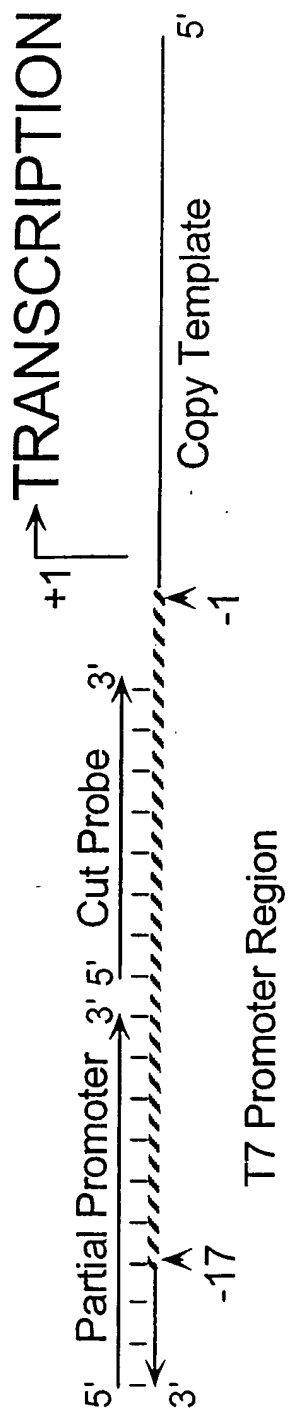
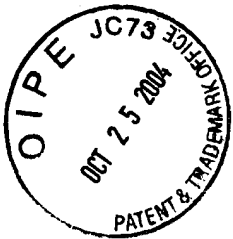
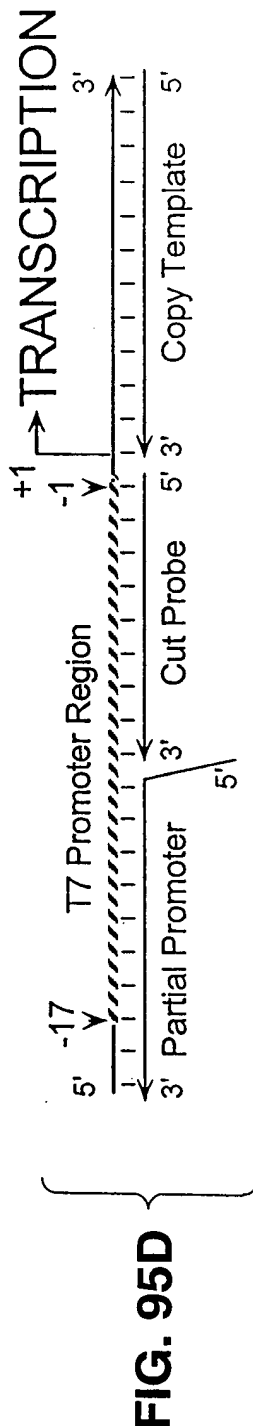
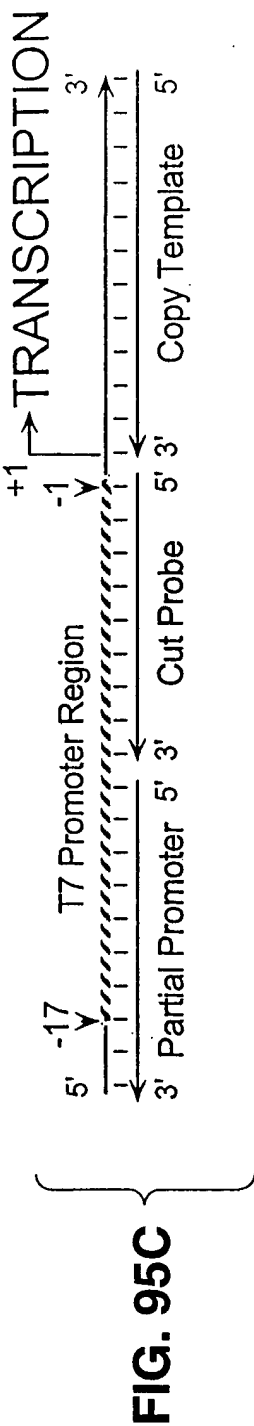
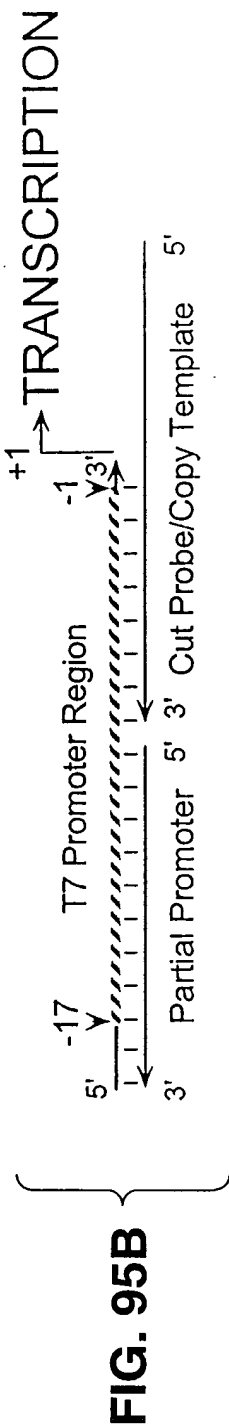
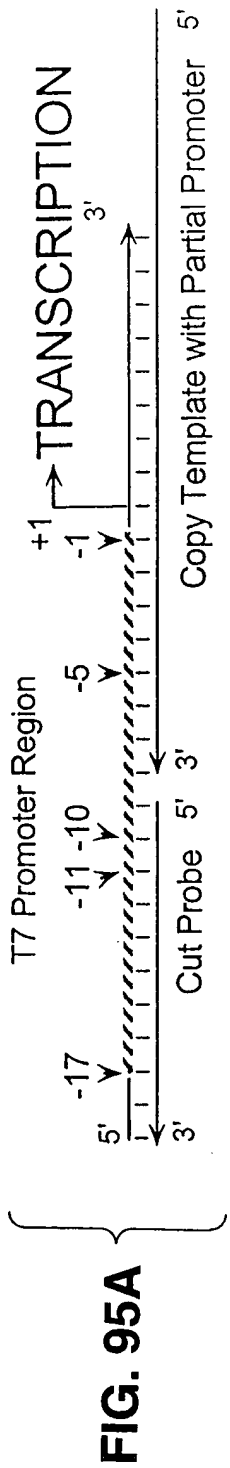


FIG. 94



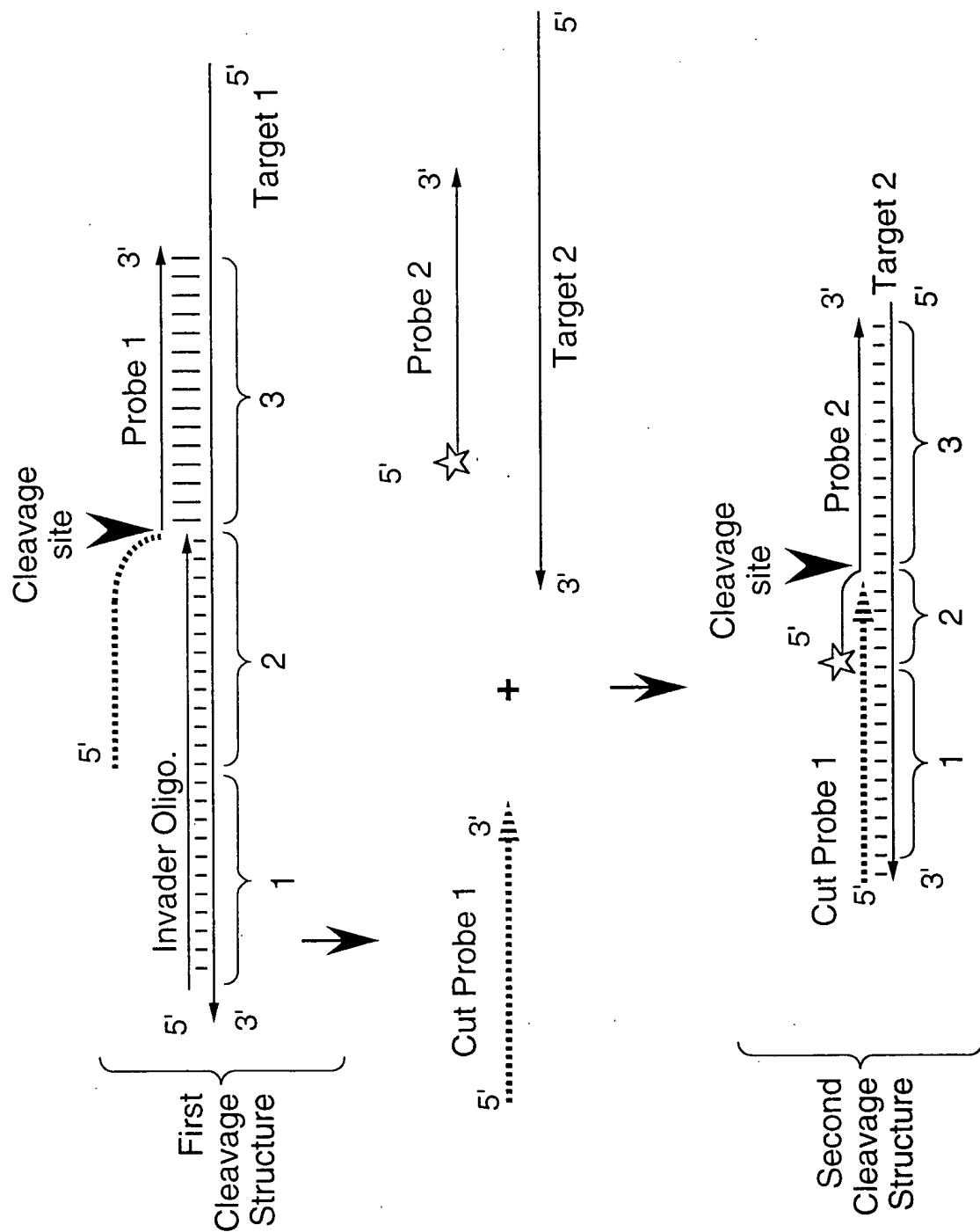


FIG. 96

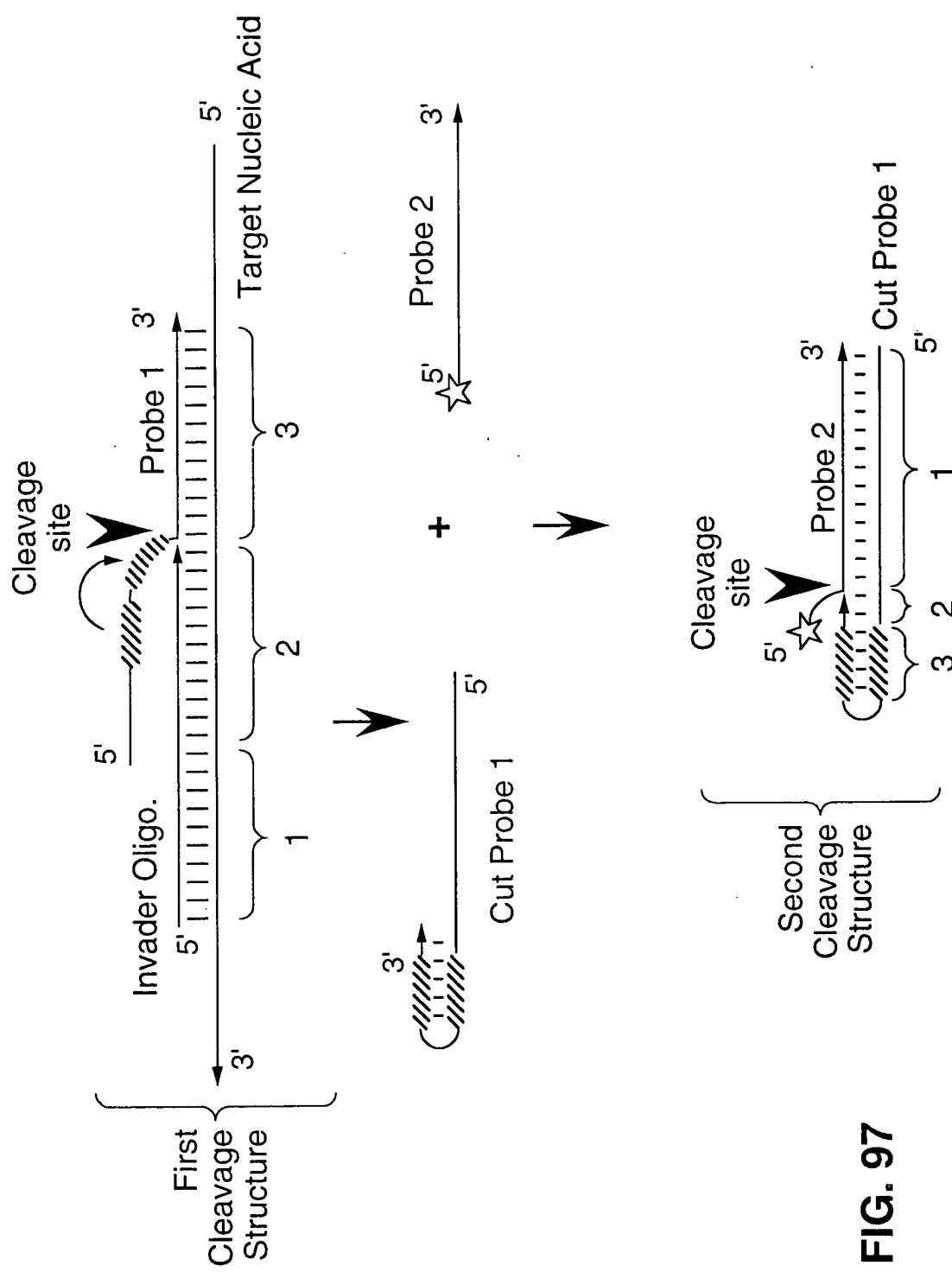
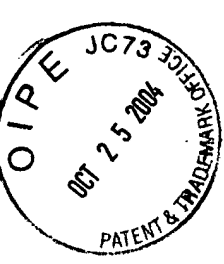


FIG. 97



PR1 probe

Cleavage site
↓
5'FITTTTCCAGAGCCTAAT G3'

IT3 Invader-Target

A^A ACGAGCGTCTTT G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A^A AGCGTCTT G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A^A CGTCTT G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A^A TCCTT G3'
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A^A CTT G3'
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

FIG. 98

FIG. 99A

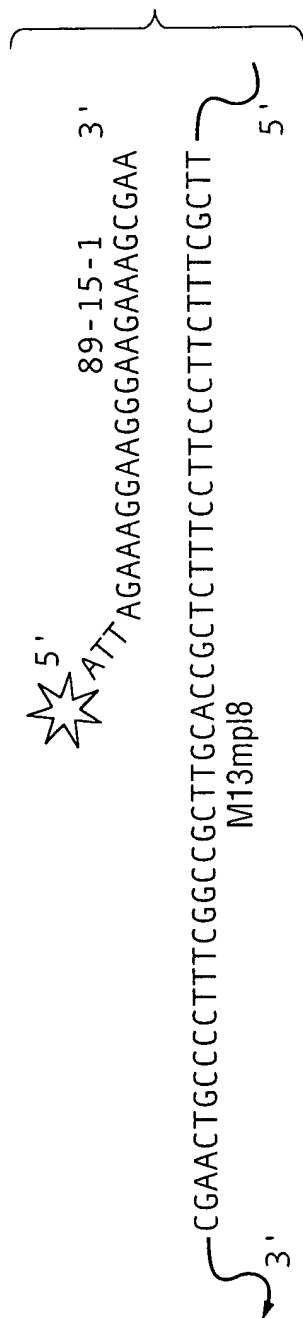


FIG. 99B

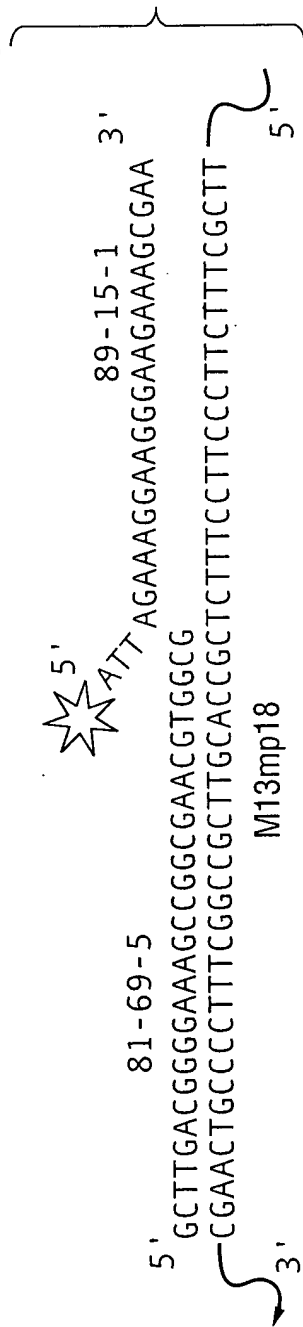
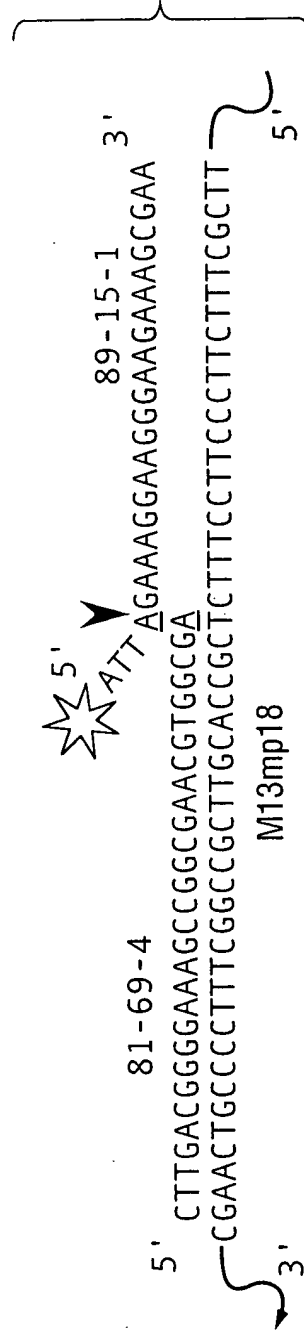
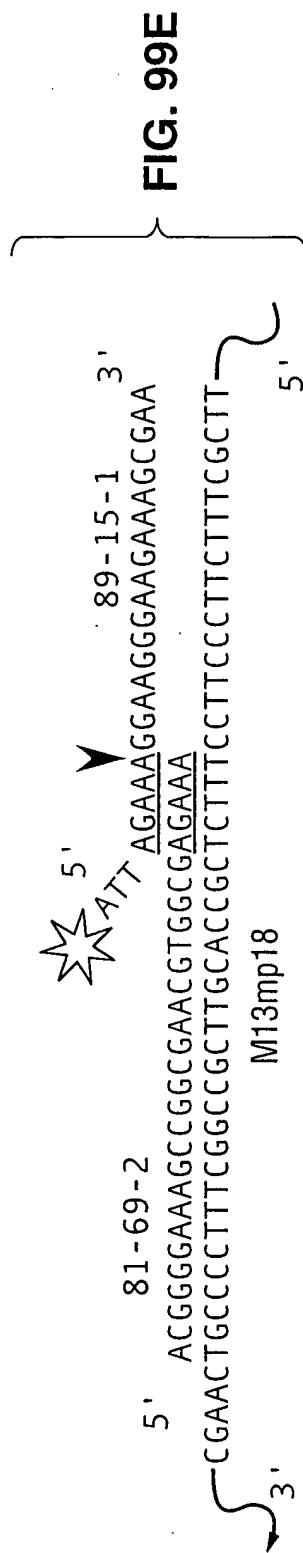
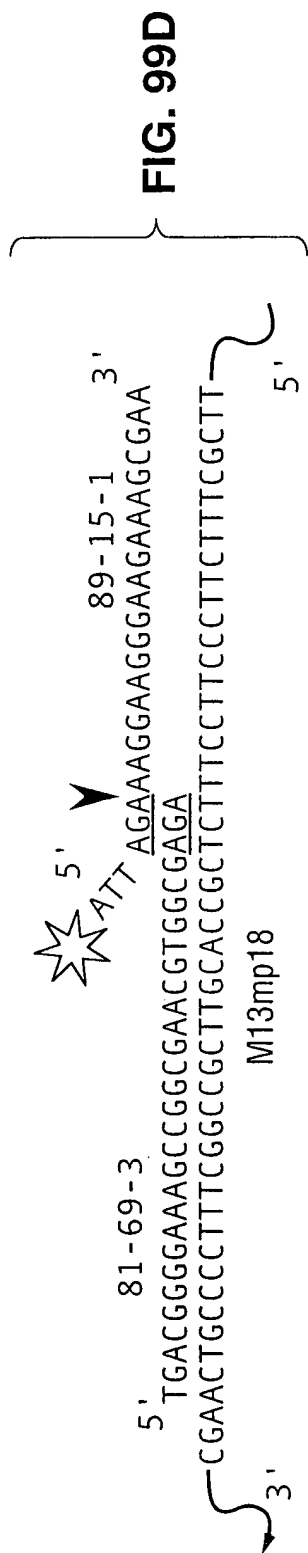


FIG. 99C





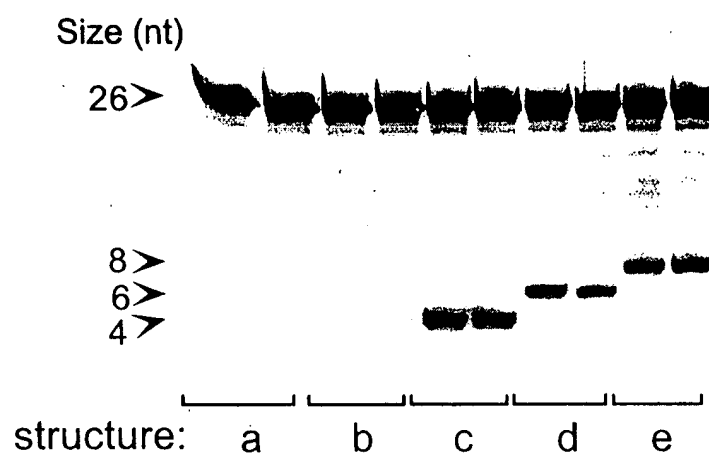
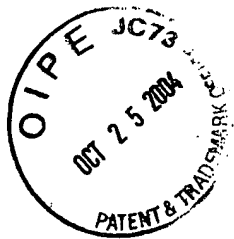


FIG. 100

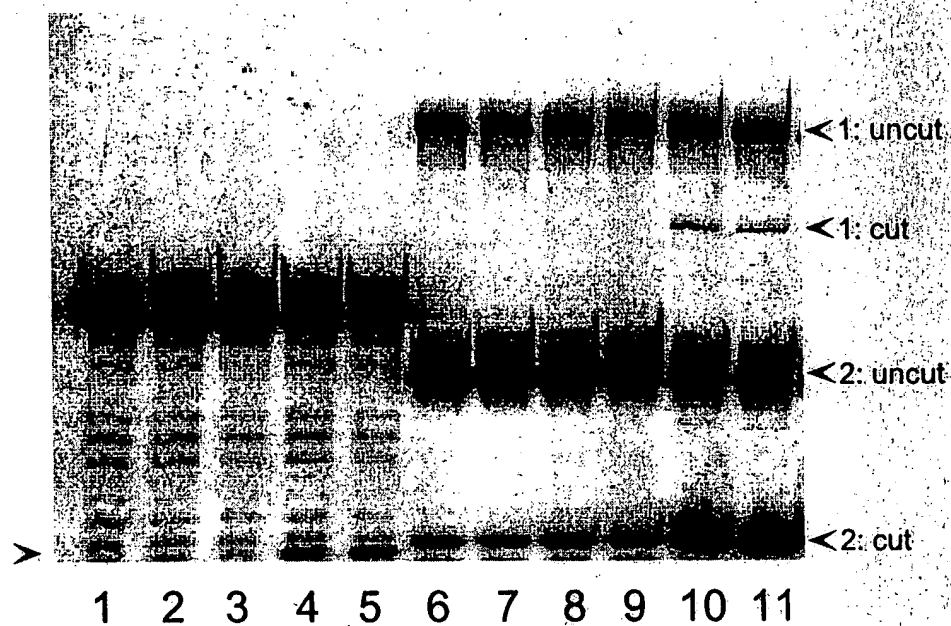
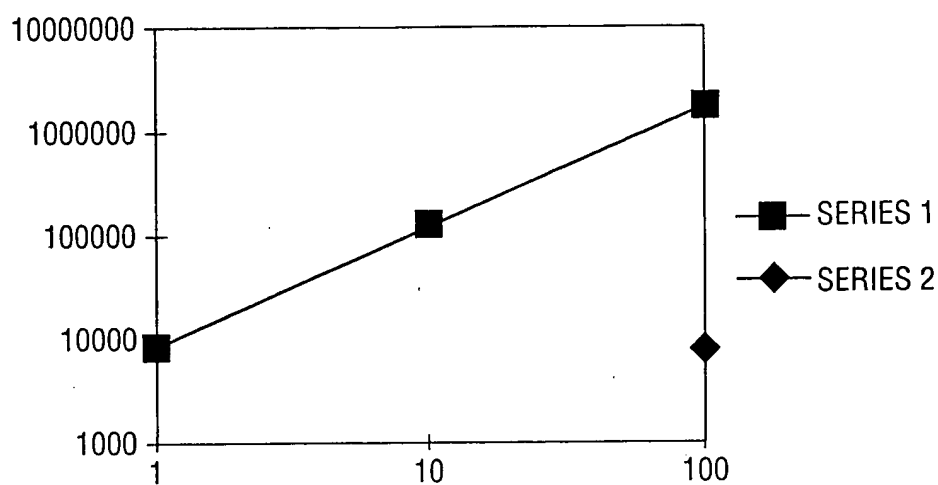
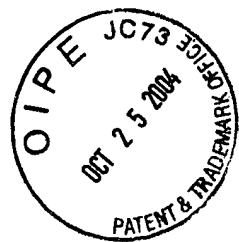


FIG. 101A



attomoles/target	basic invader	invader sqrd
1		8386
10		133185
100	8512	1862211

FIG. 101B

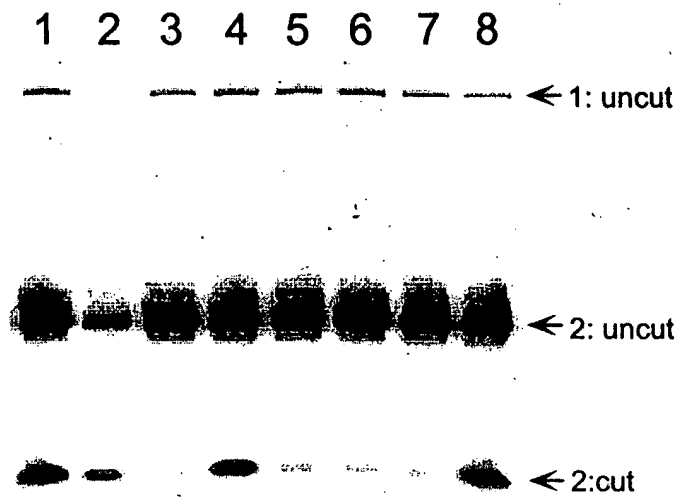
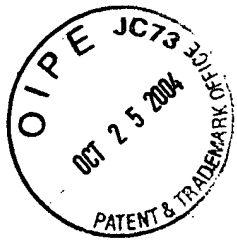


FIG. 102

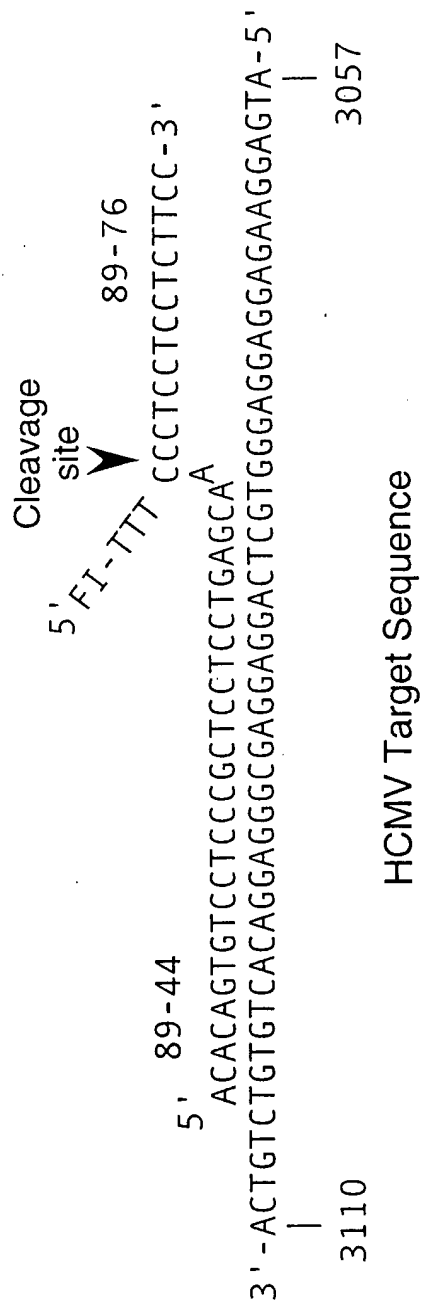
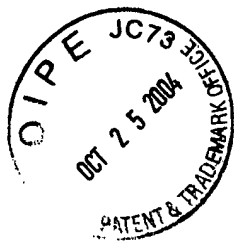


FIG. 103

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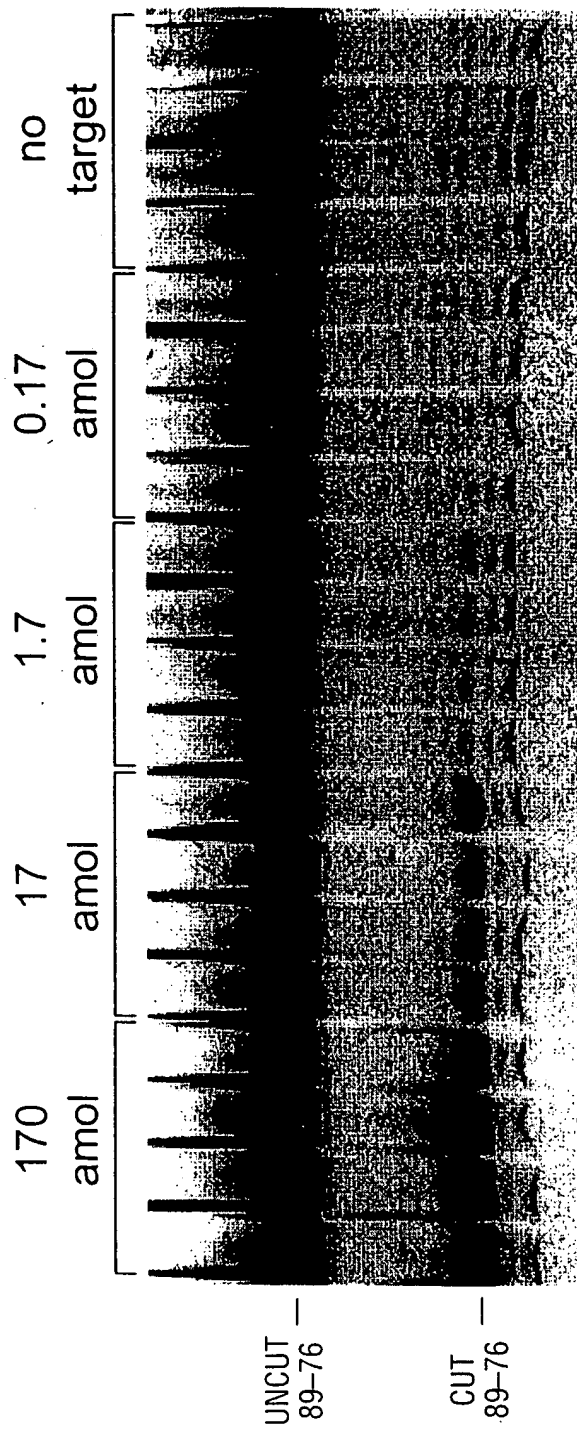


FIG. 104

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